



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 141074

TO: Andrew D Kosar
Location: REM/3C04/3C18
Art Unit: 1654
Monday, January 03, 2005

Case Serial Number: 10/800179

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
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barbara.obryen@uspto.gov

Search Notes

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STIC-Biotech/ChemLib*141074*

From: Kosar, Andrew
Sent: Wednesday, December 22, 2004 3:47 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/800,179

Please search SEQ ID NO:19 in Application 10/800,179.

The claim is drawn to proteins 'comprising' SEQ ID NO:19.

Thank you,
Andrew Kosar

*Andrew D. Kosar, Ph.D.
Art Unit 1654
Office REMSEN 3C04
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(571)272-0913*

RECEIVED
DEC 22 2005
ECM/CHIEF, Division
(STIC)

12/22/04

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Db 694 GVGVPGVGPKGVPGVGVPGVPGVAGAGAGSGAGAGSGAGAGSGVGVPG 753
QY 679 VGVPGVGVGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
Db 754 VGVPGVGVGVPGVPGVGVPGVPGVPGVAGAGSGAGAGSGAGAGSGV 813
QY 725 GVPGVGVPGVGVGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
Db 814 GVPGVGVPGVGVGPKGVPGVPGVPGVPGVPGVAGAGSGAGAGS 863

RESULT 4

AAM53541
ID AAM53541 standard; protein; 884 AA.

AC AAM53541;

DT 10-AUG-1998 (first entry)

DE Expected amino acid sequence of pPT0345 encoding SELP8K polymer.

XX Polymer SELP8K; peptide repeat unit; DNA repeat unit;

KW high molecular weight polymer; synthetic silk; silk worm.

XX Synthetic.

OS WO9810063-A1.

PN 12-MAR-1998.

PD 23-SEP-1996; 96WO-US015306.

PF 03-SEP-1996; 96US-00707237.

PR (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

PI Ferrari FA, Cappello J, Criseman JW, Dorman MA;

XX WPI, 1998-193613/17.

XX Preparation of synthetic repetitive DNA - useful for construction of
PT large protein polymers having repeating units, used in structural
PT material, e.g. synthetic silk.

XX Example 7; Page 89; 127pp; English.

XX This is the amino acid sequence of pPT0345 comprising the SELP8K protein,
CC used in the method of invention, which involves the preparation of
CC synthetic DNA sequence having repeating units from about 3-15 codons and
CC encoding a protein of at least about 30 kDa. The method is useful for the
CC production of high molecular weight polymers (e.g. synthetic silk),
CC either nucleic acids or peptides that are the expression products of the
CC nucleic acids and particularly high molecular weight peptides containing
CC repeating units which are useful structural materials

XX Sequence 884 AA;

QY Query Match 82.6%; Score 3448; DB 2; Length 884;

Db Best Local Similarity 90.6%; Pred. No. 5.7e-217;

Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58

Db 34 GAGSGAGAGSGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGAGAGSAGA 93

QY 59 GSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 114

Db 94 GSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 153

QY 115 GAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGA 170

Db 154 GAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGA 213

QY 171 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227

Db 214 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 273

QY 228 -PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG- 283

Db 274 VPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG- 333

QY 284 PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-P 340

Db 334 PGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVGVP 393

QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGKGVPGVG-PG 397

Db 394 GVGPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPG 453

QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV 454

Db 454 VGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGK 513

QY 455 G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGK 510

Db 514 GVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGV 573

QY 511 VPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGV 566

Db 574 VPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGV 633

QY 567 PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGV 622

Db 634 PGVPGKGVPGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGV 693

QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPG 678

Db 694 GVGPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPG 753

QY 679 VGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGV 734

Db 754 VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGV 813

QY 735 GVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780

Db 814 GVPGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGAGAGSGAGAGS 863

RESULT 5

AAM49728
ID AAM49728 standard; protein; 884 AA.

XX AAM49728;

AC 25-MAR-2003 (revised)

DT 12-OCT-1998 (first entry)

XX SELP8K polymer.

XX Protein polymer; SELP8K; silk-like protein; fibroin; elastin; adhesive;

KW sealant; wound healing; transglutaminase; cross-linking.

XX Synthetic.

PN US5773577-A.

Db 30-JUN-1998.

QY 02-MAR-1995; 95US-00397633.

PR 03-MAR-1994; 94US-00205518.

PI (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Cappello J;

XX
DR WPI; 1998-387091/33.
PT New recombinant protein polymers - containing naturally occurring
PT repetitive units for crosslinking by enzymes, useful as medical adhesives
PT and sealants, depots and matrices.
XX
XX Example 7; Col 43; 70pp; English.
PS
CC SELP8K polymer is a synthetic silk-like protein comprising multiple
CC copies of a monomer (see AAW9726) consisting of repeating units of silk-
CC like sequences (GAGAGS) and elastin-like sequences (VPGVG) including a
CC reactive lysine residue. It was expressed in *Escherichia coli* from
CC plasmid pPT0345 as a 80 kDa protein. The SELP8K polymer was specifically
CC designed to be functionalised with different reagents reactive to amines.
CC Claimed recombinant protein polymers are capable of covalent crosslinking
CC by enzymatic reaction to form products which set quickly and have good
CC adhesive properties and high strength. The proteins can comprise a
CC repetitive amino acid backbone of repetitive units having collagen,
CC fibroin, elastin or keratin motifs and at least 2 enzyme recognition
CC sequences comprising a glutamine or lysine capable of enzyme catalysed
CC isopeptide formation. The products can be used as medical adhesives and
CC sealants, in the closure of wounds and repair of damaged tissue. (Updated
CC on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 2; Length 884;
Best Local Similarity 90.6%; Pred. No. 5.7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 153
QY 115 GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGA 213
QY 171 GAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG 273
QY 228 -PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VFGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG- 333
QY 284 PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-P 340
DB 334 PGVGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG- 393
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 397
DB 394 GVGPGVGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 453
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGV 454
DB 454 VGVPGVGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG 513
QY 455 G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGK 510
DB 514 GVPGVGVPGVGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVG 573
QY 511 VGVGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGV 566
DB 574 VVGKGVPGVGVPGVGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGVGV 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPG 622

DB 634 PGVGVPGKGVPGVGVPGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGV 693
QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPG 678
DB 694 GVGPGVGVPGKGVPGVGVPGVGVPGVPGAGAGSGAGAGSGAGAGSGV 753
QY 679 VGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 754 VGVPGVGVPGVPGKGVPGVGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGV 813
QY 735 GVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
DB 814 GVPGVGVPGVGVPGVGVPGKGVPGVGVPGVPGVPGVPGAGAGSGAGAGS 863

RESULT 6
AA51882
ID AAY51882 standard; protein; 884 AA.

AC AAY51882;

DT 22-JUN-2000 (first entry)

DE Plasmid pPT0345 protein fragment containing SELP8K polymer units.

XX Crosslinked protein; fibrin glue; tissue adhesive; sealant; SELP8K.

XX Synthetic.

PN US6033654-A.

PD 07-MAR-2000.

PF 02-MAY-1996; 96US-00642246.

PR 05-MAY-1995; 95US-00435641.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

PI Cappello J, Stedronsky ER;

DR WPI; 2000-255682/22.

PT Crosslinked protein composition, useful as tissue adhesive or sealant,
PT comprises peptide repeating units that contain functional groups reactive
PT with crosslinker.

PS Example 2; Col 51-56; 45pp; English.

CC This invention describes a novel crosslinked protein composition (A) in
CC which, before crosslinking, the protein (I) is new and comprises at least
CC 70 wt.% of repeating units GAGAGS (1) and GVGVP (2), and in at least two
CC repeating units an amino acid (aa) is substituted by Lys or Arg to
CC provide a Lys/Arg equivalent weight of 1-20 kD. (I) contains at least two
CC aa having a functional group reactive with at least one of aldehyde,
CC iso(thio)cyanate and activated carboxy. (I) have similar biocompatibility
CC to fibrin glues, but set more quickly and give a bond with greater shear
CC strength. They are made from readily available natural sources, are easy
CC to administer and are gradually resorbed. This sequence represents a
CC crosslinking protein polymer unit designated SELP8K

SQ Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 3; Length 884;
Best Local Similarity 90.6%; Pred. No. 5.7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 114

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Db 94 GSAGAGSAGAGSGVGVPGVPGVPGKGPVGVPGVPGVPGVPGAGAGS 153
Qy 115 GAGAGSAGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -PGVG -PGA 170
Db 154 GAGAGSAGAGSGAGSGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGA 213
Qy 171 GAGSGAGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -PGVG 227
Db 214 GAGSGAGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGVPGVPGV 273
Qy 228 -PGAGAGSAGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -283
Db 274 VPAGAGSGAGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGVPGV 333
Qy 284 PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVG -PGVG -P 340
Db 334 PGVGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGV 393
Qy 341 GVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PG 397
Db 394 GVGPGVGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPV 453
Qy 398 VG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGKGPV 454
Db 454 VGVPGVPGVGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGK 513
Qy 455 G -PGVG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPG 510
Db 514 GVPGVGVPGVGVPGVGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGV 573
Qy 511 VPGVG -PGVG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPG 566
Db 574 VPGKVPGVGVPGVGVPGVPGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGV 633
Qy 567 PGKVPVPGVG -PGVG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGV 622
Db 634 PGVGVPGKVPVPGVGVPGVPGVPGAGAGSGAGSGAGSGAGSGVGVPGV 693
Qy 633 GVGVPVGVPGVGV -PGVG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSG 678
Db 694 GVGVPVGVPGKVPVGVPGVGVPGVPGVPGAGAGSGAGSGAGSGAGSGV 753
Qy 679 VGVPGVGVPGKVPVGV -PGVG -PGVG -PGVG -PGAGAGSGAGSGAGSGAG 734
Db 754 VGVPGVGVPGVGVPGKVPVGVPGVGVPGVPGVPGAGAGSGAGSGAGSGAG 813
Qy 735 GVPGVGVPGVGVPGKVPVGV -PGVG -PGVG -PGVG -PGAGAGSGAGAGS 780
Db 814 GVPGVGVPGVGVPGVGVPGKVPVGVPGVGVPGVPGAGAGSGAGAGS 863

RESULT 7
ABG31412
ID ABG31412 standard; protein; 884 AA.
XX
AC ABG31412;
XX
DT 29-NOV-2002 (first entry)
XX
XX SERP8K polymer encoded by plasmid pPT0345.
XX
XX Protein polymer; functional group; crosslink; filling; tissue;
XX tissue mass; tissue bonding; resorbable bond; flexible bond; sealant;
XX adhesive; wound healing; burn dressing; blood flow; ruptured vessels;
XX artery; vein; structural protein; vulnerrary; fibroin; elastin; collagen;
XX keratin; SERP8K.
XX
OS Unidentified.
OS Synthetic.
XX
XX US6423333-B1.
XX
XX 23-JUL-2002.
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XX
PF 29-NOV-1999; 99US-00451206.
XX
PR 05-MAY-1995; 95US-00435641.
PR 02-MAY-1996; 96US-00642246.
XX
XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Stredcomsky ER, Cappello J;
XX
DR WPI, 2002-672937/72.
XX
XX Crosslinked protein composition used as sealant or adhesive for sealing
PT or filling defect in viable tissue, as burn dressing, or in wound healing
PT e.g. to staunch flow of fluid e.g. blood, through ruptured vessels.
XX
PS Example 2; Col 17; 46pp; English.
XX
XX The present invention relates to protein polymers having repetitive units
CC from naturally occurring structural proteins such as fibroin, elastin,
CC collagen and keratin. The polymers comprise a functional group which can
CC be chemically crosslinked with appropriate crosslinkers. The protein
CC polymer is produced by recombinant DNA technology. The protein polymer is
CC useful for sealing or filling a defect in viable tissue, particularly for
CC augmenting tissue mass. The protein polymer is useful in a variety of
CC applications related to their physical, chemical and biological
CC properties, and/or to bond together separated tissue to provide a stable,
CC flexible or resorbable bond. The protein is particularly useful as a
CC sealant or adhesive, in wound healing or as a burn dressing e.g. to stop
CC or staunch the flow of fluid (e.g. blood) through ruptured vessels (e.g.
CC arteries or veins). The present sequence represents SERP8K polymer
XX
SQ Sequence 884 AA;
XX
Query Match 82.6%; Score 3448; DB 5; Length 884;
Best Local Similarity 90.6%; Pred. No. 5, 7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
XX
Qy 3 GAGSGAGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -PGVG -PGAGAGS 58
Db 34 GAGSGAGAGSGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGAGAGS 93
Qy 59 GSGAGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -PGVG -PGAGAGS 114
Db 94 GSGAGAGSGAGSGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGAGAGS 153
Qy 115 GAGAGSGAGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -PGVG -PGA 170
Db 154 GAGAGSGAGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGVPGVPGVPGA 213
Qy 171 GAGSGAGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -PGVG 227
Db 214 GAGSGAGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGVPGVPGV 273
Qy 228 -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -PGVG -283
Db 274 VPAGAGSGAGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGVPGV 333
Qy 284 PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PGVG -P 340
Db 334 PGVGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPVGVPGV 393
Qy 341 GVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGKGPVGVG -PG 397
Db 394 GVGVPVGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGKGPV 453
Qy 398 VG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGKGPV 454
Db 454 VGVPGVGVPGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGVPGK 513
Qy 455 G -PGVG -PGVG -PGVG -PGAGAGSGAGSGAGSGAGSGVGVPGVPGVPG 510
Db 514 GVPGVGVPGVGVPGVPGAGAGSGAGSGAGSGAGSGVGVPGVPGVPGVPGV 573
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QY 511 VPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGVPGVPGVPGV 566
DB 574 VPGKGVPGVPGVPGVPGVPGAGAGSAGAGSAGAGSGVPGVPGVPGV 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGVPGVPGV 622
DB 634 PGVPGKGVPGVPGVPGVPGVPGAGAGSAGAGSAGAGSGVPGVPGV 693
QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGVPGV 678
DB 694 GVGPGVPGKGVPGVPGVPGVPGVPGAGAGSAGAGSAGAGSGVPGV 753
QY 679 VGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGV 734
DB 754 VGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSAGAGSGV 813
QY 735 GVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGS 780
DB 814 GVPGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSAGAGS 863

RESULT 8

ABM01628
ID ABM01628 standard; protein; 884 AA.

AC ABM01628;

DT 12-FEB-2004 (first entry)

DE Plasmid pPRO345 SBLP&K polymer protein.

KM Crosslinked protein; sealant; depot; drug; therapy; gel; film; thread;
coating; vulnary.

OS Unidentified.

PN US2003104589-A1.

PD 05-JUN-2003.

PF 05-APR-2002; 2002US-00117931.

PR 05-MAY-1995; 95US-00435641.

PR 02-MAY-1996; 96US-00642246.

PR 29-NOV-1999; 99US-00451206.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

PI Stedronsky ER, Cappello J;

DR WPI; 2003-829350/77.

PT Crosslinked protein composition useful as sealing a defect in tissue, the
protein prior to crosslinking comprises repetitive units of 3-15 amino
acids of natural structural protein.

PS Example 2; Page 27-29; 0pp; English.

CC The present invention relates to crosslinked protein composition. The
invention is useful as sealants or depots to provide for relatively
uniform release of a physiologically active product e.g., drug and for
the formation of articles of manufacture such as gels, films, threads,
coatings. The present sequence is plasmid pPRO345 SBLP&K polymer protein
SQ Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 7; Length 884;
Best Local Similarity 90.6%; Pred. No. 5.7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGS 58
|||||

DB 34 GAGSGAGAGSGVPGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGS 93
QY 59 GSAGAGSAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSAGAGSAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 153
QY 115 GAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGA 213
QY 171 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 273
QY 228 -PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VPAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG- 333
QY 284 PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-P 340
DB 334 PGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-P 393
QY 341 GVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG-PG 397
DB 394 GVGPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVG 453
QY 398 VG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV 454
DB 454 VGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPG 513
QY 455 G-PGVG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGV 510
DB 514 GVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGV 573
QY 511 VPGVG-PGVG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGV 566
DB 574 VPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGV 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGVPGV 622
DB 634 PGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGV 693
QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGVPGV 678
DB 694 GVGPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGV 753
QY 679 VGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGVPGV 734
DB 754 VGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSGAGAGSGAGAGSGV 813
QY 735 GVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGS 780
DB 814 GVPGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGS 863

RESULT 9

AAP82961
ID AAP82961 standard; protein; 2257 AA.

AC AAP82961;

DT 25-MAR-2003 (revised)

DT 27-NOV-1990 (first entry)

DE SEPL3 protein completing gagage of silk fibroin and gvygp of elastin.

KM Repeat unit; collagen; keratin; immunisation; monomer; silk-like-protein;

KM SELF3; PSY1397; Bombyx mori; silk fibroin; elastin.

OS Synthetic.

FT Key Location/Qualifiers
Region 38..49

FT	/label= repeat_region
FT	/note= "gagags"
FT	38. .43
FT	/label= repeat_unit
FT	/note= "gagags found in natural elastin"
FT	50. .2260
FT	/label= repeat_region
FT	/note= "(gvyvp)8 (gagags)8"
FT	50. .89
FT	/label= repeat_region
FT	/note= "vpvgv"
FT	50. .54
FT	/label= repeat_unit
FT	/note= "vpvgv found in silk fibroin protein"
FT	90. .137
FT	/label= repeat_region
FT	/note= "gagags"
FT	2161. .2201
FT	/label= repeat_region
FT	/note= "vpvgv"
FT	2202. .2231
FT	/label= repeat_region
FT	/note= "gagags"

PN M08803533-A.
 XX
 PD 19-MAY-1988.
 XX
 PP 29-OCT-1987; 87WO-US002822.
 XX
 PR 04-NOV-1986; 86US-00927258.
 XX
 PA (SYTR) SYNTRO CORP.
 XX
 PI Ferrari FA, Richardson C, Chambers J, Causey SC, Pollock TJ;
 DR WPI, 1986-147587/21.
 XX
 PT DNA encoding oligopeptide repeating unit - used for producing silk-like-
 PT protein, collagen, Keratin or peptide(s) for immunisation.
 XX
 PS Disclosure; Page 7; 5pp; English.

CC The SERP sequence present in PSY1377 encodes a protein of MM168, 535. The
CC repeating unit gagaga is found in naturally occurring silk fibroin
CC protein. SILK-like proteins mimic the composition and physical properties
CC of silk of Bombyx mori. The repeating unit gysgv is found in naturally
CC occurring elastin The protein mimics the properties of elastin and
CC provides for elasticomeric properties. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 2257 AA;

Query Match	79.0%;	Score 3296;	DB 1;	Length 2257;
Best Local Similarity	67.4%;	Pred. No. 8.8e-207;		
Matches 755; Conservative	0;	Mismatches 25;	Indels 340;	Gaps 52;

[illegible][illegible]

RESULT 10
 AAR41012
 ID AAR41012 standard; protein; 2257 AA.
 XX
 XX AAR41012;
 AC
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-1994 (first entry)
 XX
 XX
 DE SLP3 multimeric protein.
 KW elastomeric protein; elastic properties; elastin-like protein.

[illegible]

```

RESULT 15
ADE44977
ID ADE44977 standard; protein, 2257 AA.
XX
AC ADE44977;
XX
DT 29-JAN-2004 (first entry)
XX
DS Recombinant structural protein SELP3 protein seq id 82.
XX
KW recombinant protein; structural component; prosthetic device;
synthetic fiber; structural protein; repeating oligopeptide; SELP3.
OS Synthetic.
XX
PN US2003083464-A1.
XX
PF 01-MAY-2003.
PD 12-MAR-2002; 2002US-00096986.
PP XX
PR 04-NOV-1986; 86US-00927258.
PR 29-OCT-1987; 87US-00114618.
PR 22-APR-1993; 93US-00053049.
PR 29-DEC-1993; 93US-00175155.
PR 07-JUN-1995; 95US-00482085.
PR 22-NOV-1999; 99US-00444791.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
CX Ferrari FA, Richardson C, Chambers J, Causey S, Pollock TJ;
PI Cappello J, Criseman JW;
PI MPI; 2003-810795/76.
DR New proteins useful as structural components of e.g. prosthetic devices
PT and synthetic fibers, comprise at least one naturally occurring repeating
PT unit of a naturally occurring structural protein.
XX
PS Example 5; SEQ ID NO 82; 107pp; English.
XX
CC The invention describes a novel recombinant protein (I) of at least 30
CC kDa comprising at least 50 percent of amino acids of at least one
CC naturally occurring repeating unit of a naturally occurring structural
CC protein, where a repeating unit comprises 3-20 amino acids, and where
CC each of the same repeating unit comprises the same amino acids. (I) has a
CC variety of uses including use as structural component of e.g. prosthetic
CC devices and synthetic fibers. The protein has the properties of a
CC naturally occurring structural protein but can be modified to have new
CC properties. This sequence represents SELP3, a recombinant structural
CC protein of the invention.
XX
SQ Sequence 2257 AA;
Query Match 79.0%; Score 3296; DB ?; Length 2257;
Best Local Similarity 67.4%; Pred. No. 8,8e-207;
Matches 755; Conservative 0; Mismatches 25; Indels 340; Gaps 52;
Db 1 GAGAGSGGAGSgvPGvGVPGvGKGVPGVG-PGVG-PGVG-PGV----- 46
38 GAGAGSGGAGSgvgPgvgVPgvgfPgvgfPgvgfPgvgfPgvgfPgvgfPgagsgga 97
47 -----GPgAgAGSGAGGSgAgAGSGAGGSgAgAGSVgPVgVPgVKgVP 92
98 GAGSGAGAGSGAGGSgAgAGSGAGGSgAgAGSVgPVgVPgVKgVP 157
Qy 93 gVg-f-gPgVg-fPgVg-fgV-----gPgAgAGSGAGSGAGA 124
Db 158 gVgVgPgVgVPgVgVgPgVgVgPgAgAGSGAGSGAGSGAGSGAGSGAGA 217
125 GSgAgAGSGgVgVPgVgVgVPgKgVPgVgVg-fPgVg-fPgVg-fPgV----- 166

```


Biochemistry 23, 9677-9683, 1990

A:Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.

A:Reference number: A36106; MUID:91104868; PMID:1702999

A:Accession: A36106

A:Molecule type: mRNA

A:Residues: 1-864 <PIR>

A:Cross-references: UNIPROT:Q99372; GB:M06047; GB:U05292; NID:g207444; PIDN:AAA42269.1;

R:Deak, S.B.; Pierce, R.A.; Belasky, S.A.; Riley, D.J.; Boyd, C.D.

J. Biol. Chem. 263, 13504-13507, 1988

A:Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.

A:Reference number: A30878; MUID:88330868; PMID:2971041

A:Accession: A30878

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 781-864 <DEA>

A:Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443

R:Frantzlan, C.; Pratt, C.A.; Farie, B.; Colaninno, N.M.; Offner, G.D.; Mogayzel Jr., P

J. Biol. Chem. 264, 15115-15119, 1989

A:Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells

A:Reference number: A36523; MUID:89359327; PMID:2768256

A:Accession: A36523

A:Molecule type: protein

A:Residues: 22-31 <FRA>

R:Rich, C.B.; Foster, J.A.

Arch. Biochem. Biophys. 268, 551-558, 1989

A:Title: Characterization of rat heart tropoelastin.

A:Reference number: S02173; MUID:89117149; PMID:2913947

A:Accession: S02173

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1P,369-545,548-764,770-864 <RIC>

A:Experimental source: heart

R:Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.

Genomics 12, 651-658, 1992

A:Title: Elements of the rat tropoelastin gene associated with alternative splicing.

A:Reference number: 154172; MUID:92241859; PMID:1572637

A:Accession: 154172

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 264-533 <RES>

A:Cross-references: GB:M6372; NID:g207455; PIDN:AAA42271.1; PID:g554527

A:Accession: 168505

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 558-864 <RE2>

A:Cross-references: GB:M6376; NID:g207459; PIDN:AAA42272.1; PID:g207462

C:Genetics:

A:Introns: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;

A>Note: the list of introns may be incomplete

C:Superfamily: elastin

C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F:1-21/Domin: signal sequence #status predicted <SIG>

F:22-864/Product: elastin #status predicted <MAT>

F:854-859/Distulfide Bonds: #status predicted

Query Match 28.4%; Score 1185; DB 1; Length 864;

Best Local Similarity 43.8%; Pred. No.5.4e-64;

Matches 378; Conservative 47; Mismatches 299; Indels 140; Gaps 57;

OY 15 GVPGV---GVPGVGPKGVPG---VGPVGVPGVPG-VGPGA-----GAG-----SGAG 57

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 23 GVPGAVPVGVP-G-GPG-GVPGAGVPGAGIGGGLGGLGPGGKPKPGAGLGAFCAG 80

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 58 AGSGAGSGAGSGAGSGVGPVGVPGVGV-----PGKVPVGVPVGVPVGVPV 106

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 81 PGGIGGAGPGAGLVSASRPGLVPGGAGAAAYKAAKAGAGIGIG-GVPGVGVG 139

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 107 GPGA-GAGSGAGSGAGSGAGSGAGSGVGP---GVGPVGVPVGPKVPVG-VGPV-G 161

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 140 VPGAIVGVGCAVAGVGTGIGLGVSTGAVVPGLGAGVGAGAGKPK-VPGVGLGVYPGG 198

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 162 VPGVG---PGAAGSGAGSGAGAG--SGAGSGVGPVGVPVGVPV---KGVPGVG 215

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

[illegible]

RESULT 6

UMMS
period clock protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
R:Accession: A24403
P:Smith, H.S.; Barciello, T.A.; Clark, B.T.; Jackson, F.R.; Young, M.W.
Nature 317, 445-448, 1985
A:Title: An unusual coding sequence from a Drosophila clock gene is conserved in vertebrates
A:Reference number: A24403; MUID:86014384; PMID:2413365
A:Accession: A24403
A:Molecule type: DNA
A:Residues: 1-713 <SH>
A:Cross-references: UNIPROT:P08399; GB:X02966; GB:M12039; NID:g55125; PIDN:CAA26710.1; F
C:Comment: Mutations within the per locus of the fruit fly affect a variety of natural b
logenous locus with multiple tandem repeats of nucleic acid hexamers (ACNGGN, TCAGGC) than
C:Comment: The serine residues of the S-G repeats found in certain proteoglycans are att
C:Superfamily: period clock protein; EGF homology
C:Keywords: circadian rhythm; tandem repeat
C:i41-77/Domain: EGF homology <EGF>

Dy 102 GGPFGPGAGAGSSGAGSAGAGSGAGAGSGGVPGVPGVGVPKGKGVG---RGV 158
Dy 144 VGVGVKPK-----VPGGLPGV-YPGVLPTGARFPGI 177
Oy 159 GPVGVPVGPGAGAGSAGAGSAGAGSAGAGSGSVGPVG-----VPGV--GVPGKG- 210
Db 178 --GVLPGVPTGAGVFKAPGGGRFA-----GIPLVGPFGQGPVPLGLPIKAP 225
Oy 211 -VPGVPGVPGVGPV---GVPRG--AGAGSAGAGSGAGAG----SGAGAGSGVGPV 259
Db 226 KLPG-GYGLPYSTGKLPGYGFGVAAGAAGAKGAPPTGTGVPQAIAAAAKAAKLXGAGA 284
Oy 260 GV-PGVGVRGAGVPVGVPVGVPVGVPVGVPVGPAAGSAGAGSAGAGSAGAGSGG----- 313
Db 285 GVLPGVGVGAAGITPG-----APGALPGTIGTAGAGADPAAAAAAAATAATYGAAGVCP 339
Oy 314 --VGVPVGVPVGVPVGKGVPGV---PGVGPVGVPVGPGAGAGSAGAGSAGAGSAGAG 370
Db 340 GVVGVPBGAGVPCGVGVPVGVPVGVPVG----- 369
Oy 371 GSGVGPVGVPVGVPVGPKGVPG--VGP-----GVPRVGP--GVPRGA 410
Db 370 -PGVGPVGVPVGVPVGIPGVGVPAGVSPAAAKAAAKAFGARGGVGGI.PTRGVGRG 428
Oy 411 GAGSGAGAGSAGAGSAGAGSAGAGSGVGVPGVGPVKGVPGVPGVPGVPGV---PGV- 467
Db 429 PPGFGDAQAQAAAAKAKKIKAG---GVGALGGLV--GAPGAI PGV-PGVGVPVGGA 481
Oy 468 PGAGGSAGAGSAGAGSAGAGSAGAGSGVGV-PGVGVP-PGVGVPKGVPVG---PGVPGVG 523
Db 482 PAAAAAARAAAAPGLGPGVGVAPGVGVARPVGVARPVGV---VPCVGVAPGVGAAPG 537
Oy 524 PGVPGAGAGSAGAGSAGAGSAGAGSGAGSGVGVPGVGPVPGKGVPGVPGVPGVG 583
Db 538 IGLPG-GVIAPAARKSAKAAKAAKAPRAAAGLP-AGVPLGLV-GVGPGL--GVGAGV- 591
Oy 584 PCVPRGAGAGSAGAGSAGAGSAGAGSGVGVPGVGPVPGKGVPGVPGVPGVG 643
Db 592 PGLAGAAPGTTLTAARAKAFAPGVGVGALGVGDLG-----GAGIPGVGGVGP--- 639
Oy 644 PGVPRGAGAGSAGAGSAGAGSAGAGSGVGVPGV---VPGKVPBGVPGVPG 701
Db 640 -----AAALGAKRAARA-AQFLGCVGVGLAVGSLGAVPG---AVELG---G 685
Oy 702 VGPGVPGAGAGSAGAGSAGAGAG-----SGAGAGSGVGP---PGVGPVGVPKGKVP 752
Db 686 VSPAAAKAAKAFGAAGCGVLAGAGRPFPIGVVAPRGRLSPIRPG-GAGSLGVGKRPX 744
Oy 753 GVGPGVPGVGPVGVPVGAGAGSGAG 777
Db 745 PFGALGALGPPG---GACLCKSCG 766

Query Match 27.2% Score 1137; DB 1; Length 713;
Best Local Similarity 35.3%; Pred. No. 3.3e-61;
Matches 257; Conservative 54; Mismatches 304; Indels 114; Gaps 14;

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QY      19 VGPVGVPVPGKGVPPGVPVGVPVGVPAGAGSGAGAGSGAGAGSG--AGAGSGCV 75  
       :|::|||  
DB      83 LSISEVGNATVEVRKTITTTGTATGATCTGTGGVKATGRGTGTDIDTDTGYTAARTVVAR 142  
  
QY      76 VPVGVPVGVPVPGKGVPPGV-GPVGVPVGVPVGVPVPGAAGSAGAGSGAGAGSGAGAGCGV 134  
       ||::|||  
DB     143 VTGTGTGTATVTETGTAKVTDGTGTGTAKVTKYAKVGTGTGTGTGTGTGTGTGTGTGT 202  
  
QY     135 GVPVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGSGAGAGSGAGAGCGV 194  
       :|::|||  
DB     203 GTAKV-----TGTDGRTGTGTGTGTGTGTGTGTGTGTGTAKVTKYTAARTVGTGT 248  
  
QY     195 GVPVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGSGAGAGSGAGAGCGV 254  
       :|::|||  
DB     249 GTAATGTGTGTGT-----GTGTGTGTGTGTGTGTGTGTAKVTKGTGTGTGTGTGTGTGT 302  
  
QY     255 GVPVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGSGAGAGSGAGAGCGV 314  
       ||::|||  
DB     303 GTGTAKVTKGT-----GTDRTGTGTGTGTGTGTGTGTGTGTGTAKVTKGTGTGTGTGTGT 354  
  
QY     315 GVPVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGSGAGSGAGAGSGV 374  
       :|::|||  
DB     355 GT-----GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 398  
  
QY     375 GVPVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGSGAGSGAGAGSG- 433  
       :|::|||  
DB     399 A-----KVLTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 444  
  
QY     434 -----VGPVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGSGAGSG 487  
       :|::|||  
DB     445 VTETGTAKVTKGTDTGTAKVTKGTGT-TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 503  
  
QY     488 AGAGSGAGV---VPGVGVPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGAG 544  
       |||::|||  
DB     504 TGTSSGSTAKVTKGTDTGTAKVTKGTGT-TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 562  
  
QY     545 GSGAGAGSGGVPPGVGPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGAG 604  
       ||::|||  
DB     563 GSGGTGTGTGTGTC-----SGSGSGTAKVTKGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 616  
  
QY     605 GSGAGAGSGGVPPGVGPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGAG 664  
       |||::|||  
DB     617 GSGGSGSGSGTGT-----GTGTGSGSGSGSGSGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648  
  
QY     665 GSGAGAGSGGVPPGVGPVGVPVPGKGVPPGVGPVGVPVPGAAGSAGAGSGAGAG 724  
       |||::|||  
DB     649 GTGTGTGTGTGTSTVTVRGTGT-----GTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 702  
  
QY      725 GSGAGAGSG 733  
       |||::|||  
DB      703 DRGTGTGTG 711
```

RESULT 7
F70806
hypothetical glycine-rich protein RV3508 - Mycobacterium tuberculosis (strain H37RV)
CSpecies: Mycobacterium tuberculosis
CDate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
CAccession: F70806
RCole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
AAuthors: Squares, R.; Sulismon, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
ATitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
AReference number: A70500; MUID:96295987; PMID:9634230
AAccession: F70806
AStatus: preliminary; nucleic acid sequence not shown; translation not shown

QY 776 AGA 778
Db 649 AAS 651

RESULT 12

A70869

hypothetical glycine-rich protein RV2490c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #ext_change 09-Jul-2004

C:Accession: A70869

R:Colo, S.T.; Broesch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70869

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1660 <COL>

A:Cross-references: UNIPROT:O53215; GB:AL021246; GB:AL123456; NID:93261507; PIDN:CAA1606

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2490c

C:Superfamily: collagen alpha 1(IV) chain

Query Match 24.8%; Score 1034; DB 2; Length 1660;
Best Local Similarity 35.5%; Pred. No. 7.9e-55;

Matches 340; Conservative 22; Mismatches 395; Indels 202; Gaps 42;

```
QY 1 GAGAGSGAGAGSGV-----VPGVPGVPGVPGKGVPGVPGVPGVPGVPGAGAGS 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 166 GAGAGSGAGAGPAGTGTGMLAGGCGVGMGAGGAGAGAGAGNAAGFAGAGAGAGAG 225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 55 GAGAGSGAGAG-----SGAGAGSGVPGV-----GVPGV-----GVPAGKGVPGV--G 95
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 226 GAG-GAGGAGAGFAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 96 PGVPGVPGVPGVPGV-----AGAGSGAGAGSGAGAGAGAGAGAGAGAGAGAGAGAG 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 DGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 149 KGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 -GDGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 202 PG-----VGPAGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 NGSMLAAGDAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 AGSGA-----GAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 461 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 278 V--GPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 EDGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 336 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 578 -GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 636
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 388 GAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 --GAG-----SGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 KGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 13

E70917

hypothetical glycine-rich protein RV1450c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #ext_change 20-Jun-2000

C:Accession: E70917

R:Colo, S.T.; Broesch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: E70917

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1329 <COL>

A:Cross-references: GB:Z95844; GB:AL123456; NID:93250713; PIDN:CA09271.1; PID:92111046

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV1450c

C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 24.2%; Score 1010.5; DB 2; Length 1329;
Best Local Similarity 33.8%; Pred. No. 1.7e-53;

Matches 340; Conservative 35; Mismatches 382; Indels 249; Gaps 47;

```
QY 1 GAGAGSGAGAGSG--VGPVPGVPGV-----VGPAGKGVPGVPGVPGVPGVPGV 40
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 GAGAGAGAGAGSGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 41 GVPAGVPGVPGVPGV-----GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 G---GVGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 GKGAGVPGVPGVPGVPGV-----GVPAGAGAG-----SGAGAGAGAGAGAGAGAG 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 GKGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 VG-----VPG--VGPVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 351 AGFAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GAGAGSGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 GKGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GAGAGSGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:51:15 ; Search time 202 Seconds

(without alignments)
2221.744 Million cell updates/sec

Title: US-10-800-179-19

Perfect score: 4173
Sequence: 1 GAGAGSGAGAGSGVGVGVG.....GVGPGVPGAGAGSGAGAGS 780

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2107.5	50.5	5263	1 FBOH_BOMMO	P05790 bombyx mori
2	1916.5	45.9	897	2 Q6Q254	Q6Q254 agelenopsis
3	1916.5	45.9	897	2 AAT08436	AAT08436 agelenopsis
4	1531	36.7	760	2 Q6PY84	Q6PY84 kukulcania
5	1531	36.7	760	2 AAT08433	AAT08433 kukulcania
6	1459.5	35.0	1002	2 Q9BIU8	Q9BIU8 argiope tri
7	1451.5	34.8	988	2 O17434	O17434 nephila cia
8	1397.5	33.5	1553	2 Q6PFR0	Q6PFR0 candida gla
9	1365	32.7	1884	2 Q9NHW2	Q9NHW2 nephila ina
10	1314	31.5	750	1 ELS_CHICK	E09716 gallus gall
11	1312.5	31.5	1713	2 Q9VTR6	Q9VTR6 drosofila
12	1302.5	31.2	912	2 Q9BIT2	Q9BIT2 plectrurus
13	1302.5	31.2	2249	2 Q9NHW4	Q9NHW4 nephila cia
14	1297.5	31.1	1953	2 Q9BIT7	Q9BIT7 nephila ina
15	1274	30.5	1729	2 Q9U617	Q9U617 drosofila
16	1230.5	29.5	907	2 Q44359	Q44359 nephila cia
17	1219.5	29.2	860	2 Q8C9L8	Q8C9L8 mus musculu
18	1218	29.2	860	1 ELS_MOUSE	P54320 mus musculu
19	1215	29.1	810	2 Q9E5Z9	Q9E5Z9 mus musculu
20	1185	28.4	864	1 ELS_RAT	Q99372 ratu
21	1159	27.8	1071	2 Q7Y048	Q7Y048 drosofila
22	1142	27.4	747	1 ELS_BOVIN	P04985 bos taurus
23	1137	27.2	672	1 PHX5_MOUSE	P08399 mus musculu
24	1136	27.2	871	2 Q44358	Q44358 nephila cia
25	1122.5	26.9	707	2 Q28098	Q28098 bos taurus
26	1120.5	26.9	679	2 Q28097	Q28097 bos taurus
27	1100	26.4	666	2 Q28096	Q28096 bos taurus
28	1100	26.4	1217	2 Q8VIY9	Q8VIY9 mycobacteri
29	1096	26.3	1901	1 PG54_MYCTU	O53553 mycobacteri
30	1094.5	26.2	992	2 Q7TWB8	Q7TWB8 mycobacteri
31	1089.5	26.1	1079	2 Q6MMW7	Q6MMW7 mycobacteri

32	1089.5	26.1	1079	2 CAE55606	CAE55606 mycobacte
33	1089	26.1	650	2 Q28099	Q28099 bos taurus
34	1087	26.0	1938	2 Q7TWC0	Q7TWC0 mycobacteri
35	1086	26.0	1715	2 Q8VI20	Q8VI20 mycobacteri
36	1084	26.0	1489	2 Q6MMW6	Q6MMW6 mycobacteri
37	1084	26.0	1489	2 CAE55607	CAE55607 mycobacte
38	1077	25.8	1460	2 Q9GUB5	Q9GUB5 gallieria me
39	1077	25.8	1468	2 Q9GUB5	Q9GUB5 nephila me
40	1041	24.9	747	1 SP01_NEPCL	SP01_NEPCL nephila cia
41	1034	24.8	1660	2 Q79FD4	Q79FD4 mycobacteri
42	1034	24.8	1660	2 CAE55496	CAE55496 mycobacte
43	1034	24.8	1660	2 Q7D721	Q7D721 mycobacteri
44	1023.5	24.5	757	2 Q75MU5	Q75MU5 homo sapien
45	1023.5	24.5	757	2 AAS07435	AAS07435 homo sapi

ALIGNMENTS

RESULT 1
FBOH_BOMMO STANDARD; PRT; 5263 AA.
AC P05790; Q17220; Q26379;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-UTL-2004 (Rel. 44, Last annotation update)
DE Fibroin heavy chain precursor (Fib-H) (H-fibroin).
GN Name=FIBH;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dioryssa; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330362; PubMed=10871375;
RA Zhou C.-Z., Confalonieri F., Medina N., Zivanovic Y., Esnault C.,
Yang T., Jacquet M., Janin J., Duguet M., Peraaso R., Li Z.-G.;
RT "Fine organization of Bombyx mori fibroin heavy chain gene.";
RL Nucleic Acids Res. 28:2413-2419(2000).
RN [2]
RP SEQUENCE OF 1-168 FROM N.A.
RX MEDLINE=80045039; PubMed=498286;
RA Tsujimoto Y., Suzuki Y.;
RT "The DNA sequence of Bombyx mori fibroin gene including the 5'
flanking, mRNA coding, entire intervening and fibroin protein coding
regions.";
RL Cell 18:591-600(1979).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=79211211; PubMed=455439;
RA Tsujimoto Y., Suzuki Y.;
RT "Structural analysis of the fibroin gene at the 5' end and its
surrounding regions.";
RL Cell 16:425-436(1979).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RX STRAIN=Kinshu X Showa;
RC MEDLINE=89094688; PubMed=3210244;
RA Mita K., Ichimura S., Zama M., James T.C.;
RT "Specific codon usage pattern and its implications on the secondary
structure of silk fibroin mRNA.";
RL J. Mol. Biol. 203:917-925(1988).
RN [5]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=94365842; PubMed=7916056;
RA Mita K., Ichimura S., James T.C.;
RT "Highly repetitive structure and its organization of the silk fibroin
gene.";
RL J. Mol. Evol. 38:583-592(1994).
RN [6]
RP SEQUENCE OF 5179-5263 FROM N.A., AND DISULFIDE BONDS.
RC STRAIN=U-139;

EX MEDLINE=99296390; PubMed=1036732;
RA Tanaka K., Kajiyama N., Ishikura K., Waga S., Kikuchi A., Ohno K.,
RT Takagi T., Mizuno S.;
"Determination of the site of disulfide linkage between heavy and
RT light chains of silk fibroin produced by Bombyx mori.";
RL Biochim. Biophys. Acta 1432:92-103(1999).
CC -!- FUNCTION: Forms the silk filament; a strong, inextensible,
CC insoluble and chemically inert fibre.
CC -!- SUBUNIT: Formed of two chains: heavy and light, that are linked by
CC a disulfide bond. Heavy-light chain assembly is essential for the
CC efficient intracellular transport and secretion of fibroin.
CC -!- TISSUE SPECIFICITY: Produced exclusively in the posterior (PSG)
CC section of silk glands.
CC -!- DOMAIN: Composed of antiparallel beta sheets. The strands of the
CC beta sheets run parallel to the fiber axis. Long stretches of silk
CC fibroin are composed of microcrystalline arrays of (-Gly-Ser-Gly-
CC Ala-Gly-Ala-)n interrupted by regions containing bulkier residues.
CC The fiber is composed of microcrystalline arrays alternating with
CC amorphous regions.

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CC
DR EMBL, AF22688; AAF76983.1; -.
DR EMBL, V00094; CAA23432.1; -.
DR EMBL, V00097; CAA23433.1; -.
DR EMBL, S74439; AAB31861.1; -.
DR EMBL, X13869; CAA32076.1; -.
DR EMBL, M35378; AAA27839.1; -.
DR EMBL, AB017362; BAA33147.1; -.
DR PIR, S01844; S01844.
KW Repeat; Signal; Silk.
KV Repeat; Signal; Silk.
FT SIGNAL 1 21 Potential.
FT CHAIN 2 5263 Fibroin heavy chain.
FT DOMAIN 149 5206 HIGHLY REPETITIVE.
FT DISULFID 5244 5244 Interchain (with light chain).
FT DISULFID 5260 5263 Interchain (with light chain).
FT CONFLICT 10 10
SQ SEQUENCE 5263 AA; 391586 MM; 8BE1D3A0A47440E CRC64;

Query Match 50.5%; Score 2107.5; DB 1; Length 5263;
Best Local Similarity 56.2%; Pred. No. 3.3e-99;
Matches 509; Conservative 6; Mismatches 234; Indels 157; Gaps 36;

QY 1 GAGAGSGAGAGSGAGV---PGVGV-----PGVGPVKGVPGVPGVPGVPGV 48
DB 2655 GAGAGSGAGAGSGAGAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGV 2714
QY 49 GAGAGSGAGAGSGAGAGSGAGVGPVGPVGPVGPVGPVGPVGPVGPVGPV 108
DB 2715 GAGAGSGAGAGSGAGAGSGAGAGSGAGA-GYGA-GAGSGAASGAGAGSGAGAGS 2772
QY 109 GAGAGSGAGAGSGAGAGSGAGAGSGVGV-PGVGV-----PGVGPVKGV 152
DB 2773 GAGAGSGAGAGSGAGAGSGAGAGVGVGVGVGVGVGVGVGVGVGVGVGV 2832
QY 153 GVGPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 202
DB 2833 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGVGV 2892
QY 203 -----GVVPGKGVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 254
DB 2893 GAGAGAGVAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 2952
QY 255 GVPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 311
DB 2953 GA-GYGA-GYGA-GYGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 3009

QY 312 SGVGV-PGVGPVGPVGPVKGV-----PGVGPVGPVGPVGPVGPVGPVGPV 363
DB 3010 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 3069
QY 364 AGSGAGAGSGVGV---PGVGPVGPVGP-GKGV-----PGVGPVGPVGPV 402
DB 3070 AGSGAGAGSGAGAGVGAAGVGA-GYGVGVGVGVGVGVGVGVGVGVGVGV 3128
QY 403 GPCVGPAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 456
DB 3129 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 3186
QY 457 GVGPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 516
DB 3187 GAGAGVGAAG 3244
QY 517 GVGPGVGP-----GVGPAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 551
DB 3245 GAGAGTGGSSGFGPYVANGVSGEYVAMSSESPFGTSGAGAGSGAGAGSGAGAG 3304
QY 552 SGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 611
DB 3305 SGAGA-----GYGA-----GVGAGYGAAGAGAGAGAGAGAGAGAGAG 3352
QY 612 SGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 671
DB 3353 SGAGA-GYGA-GAG-----SGTSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 3404
QY 672 SGVGPV-PGVGPVGPVGPVKGV---PGVGPVGPVGPVGPVGPVGPVGPV 727
DB 3405 SGVAGV 3464
QY 728 AGAGSGVGV-----PGVGV---PGVGPVGPVGPVGPVGPVGPVGPVGPV 774
DB 3465 AGAGSGAGAGSGAGAGSGAGAGAGVGA-GYGVGVGVGVGVGVGVGVGVGV 3523
QY 775 GAGAGS 780
DB 3524 GAGAGS 3529

RESULT 2
ID 060294 PRELIMINARY; PRT; 897 AA.
AC 060294;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Major ampullate spidroin (Fragment).
OS Agelenopsis aperta (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
OX NCBI_TaxID=6908;
RN [1]
RP SEQUENCE FROM N.A.
RA Tian M., Liu C., Lewis R.;
RT "Analysis of Major Ampullate Silk cDNAs from Two Non-Ord-Weaving
RT Spiders.";
RL Biomacromolecules 0:0-0(2004).
DR EMBL; AY566305; AAT08436.1; -.
FT NON_TER 1
SQ SEQUENCE 897 AA; 70174 MM; FA76E3AE802E60 CRC64;

Query Match 45.9%; Score 1916.5; DB 2; Length 897;
Best Local Similarity 50.8%; Pred. No. 5e-90;
Matches 435; Conservative 66; Mismatches 207; Indels 149; Gaps 31;

QY 1 GAGAGSGAGAGSGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 60
DB 5 GAGAGSGAGAGSGAGAGSGAGAGSGGTGA-GRGA-GLGAGLGSVGTGAAGAGAGSGA 61
QY 61 GAGAGSGAGAGSGVGV-----PGVGV-PGVGV-PGVGPVGPVGPVGPVGPV 107

DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Major ampullate spider 1 (Fragment).
OS Kukulcania hibernalis (Southern house spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Haplogynae; Filistatidae; Kukulcania.
OX NCBI_TaxID=268415;
RN [1]
RP
RP SEQUENCE FROM N.A.
RA Tian M., Liu C., Lewis R.;
RT "Analysis of Major Ampullate Silk CDNAs from Two Non-Ord-Weaving
RT Spiders".
RL Biocomolecules 0.0-0(2004).
DR EMBL; AY571308; AY108433.1; --
FT NON_TER 1
FT NON_TER 1
FT NON_TER 760
SO SEQUENCE 760 AA; 59989 MW; D98439784D9A2ABD CRC64;

Query Match 36.7%; Score 1531; DB 2; Length 760;
Best Local Similarity 46.3%; Pred. No. 1.4e-70;
Matches 401; Conservative 37; Mismatches 224; Indels 204; Gaps 33;

```

QY      2  AGAGSGAGAGSGSVGVPGVGVPGKGVPGVGVPGVGVPGVGPAGAGSGAGAGSG 61
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      11  ASAAAAAGAGSGRRPG-----GARSRCAGAGAGAGSGVG-GYSGSGAGAGAGAG 63
QY      62  AGA-----GSAGAGSGGVPGVGVPGVGVPGK-----VPGVGPVPG 101
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64  AGCEGCGFEGCGYGAAGAGGYAGAG--GRRGGRGCEAFASASSASSAVVPESAGAG 121
QY      102 VPGVGPAGAGSGAGAGSGAGAGSGAGAGSGSVGVPGVGVPGVGPBK----- 150
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

QY 151 ---VPGVPGVPG-VPGVGPAGAGSGAGSGC-----AGAGSGAGSGGVV 196

QY
197 PGVGVPGVGVPGKGVPGVEPVGVPVGPGVGPAGAGSAGAGSAGAGSGAGSSGVV 256

QY

257 258 259	PGVGVPGVGPBGVGPBGVGPBGAGAGSAGAGSAGAGSGGVC	316
-------------------	--	-----

QY PGVGPVGVPBGK-----VPGVPGVPG--VGPVGPGAGAGSGAGSSG 361
317 : : : : :
318 : : : : :
319 : : : : :
320 : : : : :
321 : : : : :
322 : : : : :
323 : : : : :
324 : : : : :
325 : : : : :
326 : : : : :
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359 : : : : :
360 : : : : :

[illegible][illegible][illegible]

DQ 530 AGAG-SGAGAGSGAGAGSGAGSGVGPVGVPKGVPGVGGPVGPVGP 588

Db 552 EEAGSSGGGSAAASAAAAGAGSGSRPG-----GARSRG-----GAGA 591

QY 589 GAGAGSGAGA-GSGAGAGSGAGAGSGVGPVGVPVGKVPVGVPVGVPVG 647

Db 592 GAGAGSSGVGGGSGGAGAGAGAGAGAG-----GEG--GFGEGCGYGAGAGAG 637

QY

648 PGAGGSGGAGCGAGAGSGAGSGGCVGVPGVGVPGVGVEKGVGVGVPGVGPVGVPGVC 707

Db AGAGAGGGSAGAGAGAGAGSAGAGGSEV-----GSGAGAGAGAGRGVG 67/9
 QY PGAGAGSAGAGAGSAGAGSAGAGSAGSVYPGYGVGVGVPPGK-----VPG 75/5
 Db AGAGAGAGAAFGSAGAGAGSAGAGAGTGAGAG-----GRGRGRGRGARFASASASAVVFE 73/3
 QY VGPVGVPGVPGVPGAGAGSGAGAG 77/9
 Db AGPGEENG--SSGDGASAAAASAAASAG 76/0

RESULT 5	
AA08433	
ID	AA08433
PRELIMINARY;	
PRT;	760 AA.

DT	12-MAY-2004 (TREMBlrel. 27, Created)
DT	12-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT	12-MAY-2004 (TREMBlrel. 27, Last annotation update)

05 *Kukulcania hibernalis* (Southern house spider).
0C Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
0C Araneomorphae; Haplogynae; Flististidae; Kukulcania.

RN [1] -
RP SEQUENCE FROM N.A.
RA Tian M., Liu C., Lewis R.;

```
RT Spiders.",
RL Biomacromolecules 0:0-0(2004).
DR EMBL; AY571308; AAT08433.1; -.
EM NCBI GenBank; AY571308.1; AAT08433.1.
```

FT	NON TER	760	760	
SQ	SEQUENCE	760 AA;	59989 MW;	D98439784D9A2A8D CRC64;
Query Match		36.7%	Score 1531.	DB 2. length 760.

2 AGAGGAGAGAGCGVGPAGVGPAGVGPAGVGPAGVGPAGVGPAGAGAGAGAGG 61
Best Local Similarity 46.3%; Pred. NO. 1.4e-10;
Matches 401; Conservative 37; Mismatches 224; Indels 204; Gaps 33

Db 11 ASAAAAAGAGSGRCRPG-----GARSRGAGAGAGAGSGVG-GYSGSGSGAGAGAGAGAG 63

Db 64 AGGEGCGFGECCGYGAGAGAGTGGAGAG --GGRGGRGCGGEARSASASASAVVFESAGAGAG 121

Db	122	AGFTGAGAGAGAGAGTGGGAGAGAGAGT	177	GRGGRGGEAFSASSASS
Qy	151	--VPGVPGTVPFG-VGPGVPGAGAGAGAGAGG	196	AGAGSGAGAGSGTGV

Db	178 A VVFESAGPGEAGSSGDDASAAASA AAAAAGSGRRGPGCARSRGAGAGAGSGVGG 237
Qy	197 PGVGVPGVGPCKGVDPGVGPVGPBGAGAGSAGAGSGAGAGSGAGSGVGV 256

Db 238 YGSG-SGAGA-----GAGAGAGAGGEGGFEGEGGCTGAGAGAGFGSGAGAGAGSGAGA 290

Db 291 -----GEGV-GSGAGAGAGAGFVGAGAGAGAGAGAGGSSGAGAGYAGAG 338

QY 317 PGVGVPGVGPKG-----VPGVGPGVGPG-VGPGVGPAGAGAGAGAGSG 361

Db 339 AG----GGRGGRGGEAFSASASSAVVFESAGPGEELAGSSCGGASAAAAGAGSG 394

QY 362 -----AGAGSAGAGSGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGAG 411

Db 395 RRGPGARSRGAGAGAGAGAGCGGTGGG-SAGA-----GAGAGAGAGGEGFGEGG 447

Db 448 YGAGGAGTSSGAGAGAGSGAGA-----GEGV-SSGAGAGAGAGVVGAGAG 495

RESULT	7		
017434			
ID	017434	PRELIMINARY;	PRT; 988 AA.
AC	017434;		
DT	01-JAN-1998 (TrEMBLrel. 05, Created)		
DT	01-JUN-1998 (TrEMBLrel. 05, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Minor ampullate silk protein MsSp1 (Fragment).		
OS	Nephila clavipes (Orb spider).		
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;		
OC	Araneomorphae; Entelegynae; Araneoidae; Tetragnathidae; Nephila.		
OX	NCBI_TaxID=6915;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98200471; PubMed=954138;		
RA	Colgin M.A., Lewis R.V.		
RT	"Spider minor ampullate silk proteins contain new repetitive sequences		
RT	and highly conserved non-silk-like 'spacer regions'."		
PL	Protein Sci. 7:667-672(1998).		
DR	EMBL; AF027735; MACE4589.1; -.		
FT	NON TER		
FT	1		
FT	1		
SEQUENCE	988 AA; 79082 MW; 461E03DF53F7085D CRC64;		

[illegible]

RESULT 9

Q9NHW2		
ID	Q9NHW2	PRELIMINARY; PRT; 1884 AA.
AC	Q9NHW2;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE	Flagelliform silk protein (Fragment).	
GN	Name=Flag;	
OS	Nephila inaurata madagascariensis.	
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;	
OC	Araneomorphae; Entelegynae; Araneoidae; Tetragnathidae; Nephila.	
OX	NCBI_TaxId=115969;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20156766; PubMed=10688794;	
RA	Hayashi C.Y., Lewis R.V.;	
RT	"Molecular architecture and evolution of a modular spider silk protein	
RL	gene.";	
RL	Science. 287:1477-1479(2000).	
DR	EMBL; AF218623; AAF36091.1; "-.	
DR	GO; GO:0005737; C:cycloplasm; IEA.	
DR	GO; GO:0006817; P:phosphate transport; IEA.	
DR	InterPro; IPR008160; Collagen.	
FT	NON_TER	1884 1884
Q0	SEQUENCE	1884 AA; 148738 MW; 27B6F45339FD20A5 CRC64;

Query Match

Best Local Similarity 42.3%; Pred. No. 6.2e-62;
Matches 412; Conservative 16; Mismatches 334; Indels 212; Gaps 65;

[illegible]

Db	479	GAAGAGGAGCGSGSTTTIEDLDTITTDGADGPTTTSBELTTTCAGACGSGPGCAGPGCVGP	538
QY	221	G-VGP-GVGP-GAAGAGSGAGAGSG-AGAGSGAGAGSGVGPVGVPVGPVPGKGVPGVGP	276
Db	539	GRSRPGCVGPGSGSRPGSVPGPGSGGCGLGLGRSRPGCVPGPGSGSRPGSLGPPGSGGCGLGP	598
QY	277	GVGPVGVPVGPVPGAGAGSGAGAG-----SGAGAGSGAGAGSGVGPVGPVGP-GVGPV	327
Db	599	G-GSGGCG-GLPGPGSGSPGVGSGGVGPGGSGPGGVGAGAGPGVYGVGSGGCGPCGAGGP	656
QY	328	-GKXVP-----GVGPVCVPG-----VGPG--VGPAGAGSGAGAGSGAGAGSGAGAGSGVGP	375
Db	657	YGPGGPYGPGGAGGYPGGAGAGGPGYGPFGCPYGPAGAGPGGGGPGGAGGPGYGPGGPGGAG	716
QY	376	VPGVGVPGVGPVPGKGVDPGVGP-GVGP-GVGP-GVPGAGAGSGAGAGSGAGAGSGAGAGSG	432
Db	717	PGGVPGGVGPFGCAGPGGAGPGGYPGGAGGCGYGP-G-GAGPG-GTGRGGSRRG	773
QY	433	GVGVPGVGPVPGVGPVPGKGVPGVGP-GVGP-GVGP-----	468
Db	774	GYGPGGCGTGGCTGPGCAGPGCAGPGCAGPGGAGPGGAGPGGAGGCGSGRGSVRGCGAGRG	833
QY	469	GAGAGSGAGAGSGAGAGSGAGAGSGVGP-----	503
Db	834	GAGRGAGAGAGAGSGAGAGSGAGAGSGGCTTTIEDLDTVDGANGPTTTSBELTTTCAGAGCG	893
QY	504	VGVPGKGVPGVGP-GVGP-GVGP-GVPGAGAGSGAGAGSGAGAGSGAGAGSGVGPVGPVGP	560
Db	894	VGPBGSGRPGVGPBGSGSRPGVGPBGSGRP-GVSG-GSGPG-GVGPBGSGRPGVGSAGRG	950
QY	561	VPGVGVPGKGVPGVGP-GVGPVGPVGP-GVPGAGAGSGAGAGSG-----AGAGSGAGAGSG	613
Db	951	PGGIGPGSGGPGGYPGVGPGGAPYVPGGSGPGCAGAGAGGSGYGPGGPYVPGGSGCGPGCAGGP	1010
QY	614	VGVPVCVGP-----GVGVGKXVPG-----VGPVGPVGPVGP-GVGPAGAGSG--	655
Db	1011	YGPBGAGCPYGPBGAPYGPBGAGGGGAGGPGCAGAPYVPGGPGGAGPGGYPGP-GAGPGCY	1065
QY	656	--AGAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGP	710
Db	1070	GPGAGRGPGVGPBGAGSGG-GYGPBGAGAPPGVGPBGPPGCGYGPBGAGAPPGVGPBGCTGPGG	1128
QY	711	GAGSGAGAGSGAGAGSGAGAGSGVGP-VGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGP	765
Db	1129	SAPGAGPG-GAGPGGVGPBGSGGCGYGPBGGPGCAGAPGAGPGCAGAPGAGPGGAGPGG	1187
QY	766	VGPAGAGSGAGAG	779
Db	1188	AGPGAGPGGAGPG	1201

RESULT 10

ELS_CHICK	STANDARD:	PRT:	750 AA.
ID_ ELS CHICK			

DT 01-ANCS-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last Sequence Update)
DT 05-JUL-2004 (Rel. 44, Last Annotation Update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=ELN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP
RX SEQUENCE FROM N.A.
FX MEDLINE=67242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning."
RL Biochemistry 26:1497-1503(1987).
NN [2]

R	P	SEQUENCE OF 85-750 FROM N.A. (ISOCORM 2).
R	X	MEDLINE=86309083; PubMed=2841924;
R	A	Baile V.J., Foster J.A.;
R	T	"Multiple chick tropoelastin mRNAs";
R	L	Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
R	N	[3]
R	P	SEQUENCE OF 457-750 FROM N.A.
R	C	TISSUE=Aorta;
R	X	MEDLINE=87297534; PubMed=3502711;
R	A	Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
R	T	"Sequence analysis of elastin cDNA from chick aorta and tissue-
R	T	-specific transcription of the elastin gene in developing chick
R	T	embryo.";
R	L	Arch. Biochem. Biophys. 256:455-461(1987).
R	C	- FUNCTION: Major structural protein of tissues such as aorta and
R	C	nuchal ligament, which must expand rapidly and recover completely.
R	C	- SUBUNIT: The polymeric elastin chains are cross-linked together
R	C	into an extensible 3D network.
R	C	- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
R	C	- ALTERNATIVE PRODUCTS:
R	C	Event=Alternative splicing; Named isoforms=2;
R	C	Comment=Additional isoforms exist;
R	C	Name=1;
R	C	IsoId=P07916-1; Sequence=Displayed;
R	C	Name=2; Synonyms=Embryonic;
R	C	IsoId=P07916-2; Sequence=VSP_004241, VSP_004242;
R	C	- PTM: The crosslinks are made of deaminated lys.
R	C	-----
R	C	This SWISS-PROT entry is copyright. It is produced through a collaboration
R	C	between the Swiss Institute of Bioinformatics and the EMBL outstation -
R	C	the European Bioinformatics Institute. There are no restrictions on its
R	C	use by non-profit institutions as long as its content is in no way
R	C	modified and this statement is not removed. Usage by and for commercial
R	C	entities requires a license agreement (See http://www.isb-sib.ch/announce/
R	C	or send an email to licenses@isb-sib.ch).
R	C	-----
D	R	EMBL; M18633; AAA48761.1; ..
D	R	EMBL; M21880; AAA49082.1; ..
D	R	EMBL; M15889; AAA49108.1; ..
D	R	PIR; A26601; A26601.
D	R	InterPro; IPRO08160; Collagen.
D	R	InterPro; IPRO03979; tropoelastin.
D	R	Pfam; PF01391; Collagen_1.
D	R	PRINTS; PR01500; TROPOLASTIN.
K	V	Alternative splicing; Connective tissue; Repeat; Signal;
K	W	Structural protein.
F	T	NON TER 1 1
F	T	SIGNAL <1 24
F	T	CHAIN 25 750 Elastin.
F	T	DOMAIN 83 686 8 X tandem repeats.
F	T	REPEAT 83 127 1.
F	T	REPEAT 219 262 2.
F	T	REPEAT 263 318 3.
F	T	REPEAT 319 393 4.
F	T	REPEAT 394 482 5.
F	T	REPEAT 483 554 6.
F	T	REPEAT 555 619 7.
F	T	REPEAT 620 686 8.
F	T	DISULFID 739 745 By similarity.
F	T	MOD_RES 63 63 Allysine (potential).
F	T	MOD_RES 66 66 Allysine (potential).
F	T	MOD_RES 111 111 Allysine (potential).
F	T	MOD_RES 115 115 Allysine (potential).
F	T	MOD_RES 156 156 Allysine (potential).
F	T	MOD_RES 159 159 Allysine (potential).
F	T	MOD_RES 198 198 Allysine (potential).
F	T	MOD_RES 200 200 Allysine (potential).
F	T	MOD_RES 235 235 Allysine (potential).
F	T	MOD_RES 252 252 Allysine (potential).
F	T	MOD_RES 256 256 Allysine (potential).
F	T	MOD_RES 297 297 Allysine (potential).
F	T	MOD_RES 301 301 Allysine (potential).
F	T	MOD_RES 354 354 Allysine (potential).

FT	MOD_RES	357	357		Alllylne (potential).
FT	MOD_RES	427	427		Alllylne (potential).
FT	MOD_RES	431	431		Alllylne (potential).
FT	MOD_RES	513	513		Alllylne (potential).
FT	MOD_RES	517	517		Alllylne (potential).
FT	MOD_RES	520	520		Alllylne (potential).
FT	MOD_RES	586	586		Alllylne (potential).
FT	MOD_RES	590	590		Alllylne (potential).
FT	MOD_RES	593	593		Alllylne (potential).
FT	MOD_RES	655	655		Alllylne (potential).
FT	MOD_RES	658	658		Alllylne (potential).
FT	MOD_RES	719	719		Alllylne (potential).
FT	MOD_RES	722	722		Alllylne (potential).
FT	MOD_RES	743	743		Alllylne (potential).
FT	MOD_RES	748	748		Alllylne (potential).
FT	MOD_RES	750	750		Alllylne (potential).
FT	VARSPLIC	212	212		G -> GLGFGGCGQGVPLGGYRKPRLPG (in isoform 2).
FT	FT			/FTId=VSP_004241.	
FT	VARSPLIC	501	501		G -> GVGVPFGVPG (in isoform 2).
FT	FT			/FTId=VSP_004242.	
FT	CONFLICT	536	536		A -> G (in Ref. 3).
FT	CONFLICT	571	571		P -> A (in Ref. 3).
FT	CONFLICT	610	610		P -> A (in Ref. 3).
FT	CONFLICT	654	654		A -> R (in Ref. 3).
FT	CONFLICT	667	667		P -> R (in Ref. 3).
SQ	SEQUENCE	750 AA;	63697 MW;	E57ECB06CBE556P CRC64;	
<hr/>					
Query Match 31.5%; Score 1314; DB 1; Length 750;					
Best Local Similarity 48.0%; Pred. No. 1,3e-59;					
Matches 398; Conservative 34; Mismatches 19; Indels 206; Gaps 64					
Oy	16	VPGV-----	-GVPGVGPQGKVPGVPGVPGVPGVPGAGAGSGA	62	
Db	9	LPLVLLFLFILPASQCGVPG-AIRGCGVP-----	-GGGFPPAGVG----	GLGA	52
Oy	63	GAGSGAGAGSGGVPGV--GVPGV-----	-VPGKVPGVPGVPG--PGV--PGVPGAGAGS	114	
Db	53	GLGGLGAGGKPLKPKPVSGTGLGLPLQLPGAVGGIAGAGAPGAAPGAASAAALKR		112	
Oy	115	GAGSGAGAGSGAGAGSGGVPGVPGVPGVPGVPGVPG--VGPVPGVPGVPGVPGAG	173		
Db	113	AARAGAALGGVGTIGLGSVG--GVGVC---	-GLVPGVVQPGVGAAGRPRKYPGAGT-	165	
Oy	174	SGAGAGSGAGAGSGAGAGSGGVPGVGV--PGVGPBGAKVPGVPGVGP-----	220		
Db	166	-----PGARPGGGVLPGAIRHPGVGVLPVPPT-GTGIRAKKGGAAGFAGIPGRYLRPF	218		
Oy	221	--GVPGVPGAGAGSG--AGAGSGAGAGSGAGSGVCPVPGV--PGVGPBGKVPVGP	276		
Db	219	VNGLGPG-GIGAIVLVLAGKAYPTGTGVGAQAAMAKAKYACAGVLPAG--GIPEGV--	272		
Oy	277	GVGVPVPGVPGVPGAGAGSGAGSGAGSGAGGA--GSGGVPGVPGVPGVPGVPGV	335		
Db	273	GVVPGV--GVPPGAVGVPAAAAAAKAARAGATGAAV-----LPGAG--GVPPGV	320		
Oy	336	PGVG--PGVGPBGV--PGAAGSGAGAGSGAGAGSGGVPGVPGVPGVPGKVP	391		
Db	321	PGVGVVGLVPGVGGI-PGV--AGVTGPAAMAAAARAKXKAGAVPGVPGVGT--GGV	375		
Oy	392	PGVGPVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGGVPGV--GVPGV--GVPGK	449		
Db	376	PGV--PGV--PGV-----	-PGVPGVPGVPGVPGV--	403	
Oy	450	GVPGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGGVPGVPGVPGVPGK	509		
Db	404	GVPGV--PGVVPBGVGV--GPPAAAAAATAA---KAAAFAGAVPGVPGV--ALVPGVPGV	457		
Oy	510	GVPGV--PGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGGVPGVPGVPGV	568		
Db	458	GVPGVGPVPGV-----	-PGVGPVPGVPGVPGVPG	486	
Oy	569	KGVPGV--PGV--PGVPGVPGVPGAGAGAGAGS--GAGAGSGAGAGSGV--VPGV--V	621		

Db 443 QTGAQDPGVGAQPPGVGAQTGAQDPGVGSQPPGVGGQTGAQDPGVGSQPPGVGAQTGAQDPG 501
 QY 302 AGAGSGAGSGSGVPGVG--VPGV-GVPBGKVPVG--PGVPGVG---PGVPGAGAGS 354
 Db 502 YGAQPGVGAQTGAQDPGVGSQPPGVGGQTGAQDPGVGTQPPGVGAQTGTQDPGVGAQPPGVGT 561
 QY 335 GAGAGS-GAGAGSGAGAGSGVGPVPGV-PGVGV-PGKGVPGV--PGVG-----PGV 402
 Db 562 QTGAQDPGVGSQPPGVGGQTGAQDPGVGTQPPGVGAQTGTQDPGVGAQPPGVGTQTAQDPGV 621
 QY 403 G--PGVG--PGAGAGSGAGAGSGAGAGSGAGSGAGSGVPGVGVP-PGV-GVPGKVPVG- 455
 Db 622 GSGPPGVGTQPPGVGAQTGTQDPGVGAQPPGVGGQTGAQDPGVGTQDPGVGGQTGAQDPGVGS 680
 QY 456 -PGVPGVG---PGVPGAGAGSGAGAGSGAGAGSGAGSGAGSGVGPVPGVPGV--GVPGK 509
 Db 681 QPVGIGQGTGGGQPPGVGSQPPGVGGQTGAQDPGS-YGSPGVGAQMGAGQPPGVGTQPPVIGGGQTGA 739
 QY 510 GVPVG--PGVG-----PGVG-----PGVPGAGAGS 534
 Db 740 GQPPGVGGQTGGSGSGFLTPGVGGISGPIGKLGCGGSEAKPPGYMAQPPVIGGSPKSYGS 799
 QY 535 GAGAGSGAGAG-SGAGAGSGV-----GVPGVG-PGVG---VPG-- 568
 Db 800 QPVGIGQGTGGGSGVGGQPPGVGGQATISGPPGVGTQPPVIGGALTRAVPGH 859
 QY 569 -----KVPVPG-----PGVG-----PGVG----- 579
 Db 860 YGYETQPPVIGQGTGTQPPGVGGQPPVIGGGQTGAQDPGVGYFTQPPVIGGGQTGTSGRQPPVGT 919
 QY 580 -PGVG-----PGVPGAGAGSGAGAGS-GAGAGSGAGAGSGVGPVPGV-PGVGVPGK 629
 Db 920 QPVGIGQGTGAQDPGVGSQPPGVGGQTGAQDPGVGSQPPVIGGGQTGAQDPGVGAQPPGVG---- 975
 QY 630 GVPVG--PGVG-----PGVG--PGVG-----PGAGAGSGAGAGSGAGAGSGAGAG 671
 Db 976 GQPPGVGNQPPVGGQGTGAQDPGVGSQPPVIGGGQTGAQDPGVGAQPPGVGGQLTGPNQPPVGGQ 1035
 QY 672 SGVGPVPGV-VPGV-----GVPGKGV-PGVG--PGVG-----PGVG--PGV--PGA 710
 Db 1036 TGAQDPGVGTQPPVGGQGTGAQDPGVGTVPVPGGGQPPVIGGGQTGAQDPGVGGQPPVIGGSPVY 1095
 QY 711 GAGSGAGAGSGAGAGSGAGSGVGPVPGVPGVG-VPG-----KVPVGPVPGVPGV 763
 Db 1096 GTQGTGGQSGISGQDPGVGTQPPVGGQGTGAQDPGVGSQPPVIGGGQTGAQDPGVGPVGGQPPVIG 1154
 QY 764 -----PGVG-----PGAGAGSGAGAG 779
 Db 1155 GQTVGAGGAGYGSQPPVIGGAPVYGTQPPVGGGQGTGVGG 1191

RESULT 12		
Q9BIT2	PRELIMINARY;	PRT; 912 AA.
ID Q9BIT2		
AC Q9BIT2;		
DT 01-JUN-2001 (TREMBLERel. 17, Created)		
DT 01-JUN-2001 (TREMBLERel. 17, Last sequence update)		
DT 01-OCT-2002 (TREMBLERel. 22, Last annotation update)		
DE Fibroin 1 (Fragment) .		
OS Plecteurys tristici (Spider)		
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;		
OC Araneomorphae; Haplogynae; Plecteuridae; Plecteurys.		
OX NCBI_Taxid:33319;		
(1)		
SEQUENCE FROM N.A.		
RP MEDLINE=21179804; Pubmed=11283372;		
RA Ganesy J., Hayashi C., Mocrink D., Woods J., Lewis R.;		
RT "Extreme diversity, conservation, and convergence of spider silk		
RT fibroin sequences.";		
RL Science 291:2603-2605 (2001) .		
(2)		
SEQUENCE FROM N.A.		
RP		

PL	RA	EMBL	Score	DB 2	Length	Indels	Gaps
Query Match	31.2%	Score 1302.5	DB 2	Length 912			
Best Local Similarity	32.8%	Pred. No. 5.8e-59					
Matches 334	Conservative	55	Mismatches 215	Indels 413	Gaps 21		
FTI	NON-TER	1					
SQ	SEQUENCE	912 AA; 74131 MW; 0A9FE14AA60D3EB5 CXC64					

[illegible]


```
QY 416 AGAGSGAGAGSGAGSGGVGVPVGV--PGV-GVPGKVPVGV--PGVGPVGV---PGVGP 468
Db 701 PGQ-PGYGTQPGVGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759
QY 469 GAGAGSGAGAGSGAGAGSGAGSGGVGVPVGV--GVPGKVPVGV--PGV-----519
Db 760 QIGGQTGAAGQPS--YSSQPGVGAONGGGQTCYGTTPYIGGQTGAAGQPGYGGQTGVGSSPGF 818
QY 520 ---PGV-----PGVPGAAGSGAGAGSGAGAG--SGAGA 550
Db 819 LTQPGIGGIGISPIGKVGGGQSEAAKPGYMAQPGIGPSRYGSQPGIDQTAGAGSGYCG 878
QY 551 GSGV-----GVPGVY--PGV-----VPG-----KGVPGV-----575
Db 879 QPGISGQTGGGQPGYGGQATISGLPGYGTQPGIGALTAVPGGHYGETQPGIGGQTGTNQ 938
QY 576 PGVGV--PGV-----PGV-----PGAGAGSG--AGAGSGAGAGSGAGSGGVGVPVGV--620
Db 939 PGFGGQPGIGGQTGAAGQPGYGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 998
QY 621 VPGV-GVPGKVPVGV--PGV-----PGV-----PGAGAGSGAGAGSG 661
Db 999 QPGIGGQTGAAGQPGYGSQTGVGGQIGAGQPGYGSQPGIGGQTGAAGQPGYGAQPGFGGQPG 1058
QY 662 AGAGSGAGAGSGGVGVPVGV--VPGV-GVPGKVPVGVPGVPGV--PGV-----PGA 710
Db 1059 YGNQPGVGGQTGAAGQPGYGSQPGVGGQTGAAGQPGY--GVIPFGGQPGIGGQTAAAGKPGY 1116
QY 711 GAGSGAGAGSGAGAGSGAGSGGV--GVPGVGV--PGVVPVKGK--VPGV-----P 756
Db 1117 GGGQPGIGSSPVYGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1176
QY 757 GVGPGVGPVGV-----PGAAGSGAGAG 779
Db 1177 GYGPSSQPGIGGAPVYGTQPGGGGQTGVIGG 1207
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Search completed: December 30, 2004, 12:54:58
Job time : 215 sec8

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[illegible]

RESULT 2
US-08-397-633A-68
; Sequence 68, Application US/08397633A

1 APPLICANT: Cappello, Joseph
2
3 TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
4
5 TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
6
7 NUMBER OF SEQUENCES: 105
8
9 CORRESPONDENCE ADDRESSES:
10
11 ADDRESSEE: FLEH, HOHBACH, TEST, ALBRITTON & HERBERT
12
13 STREET: 4 Embarcadero Center, Suite 3400
14
15 CITY: San Francisco
16
17 STATE: California
18
19 COUNTRY: USA
20
21 ZIP: 94111-4187
22
23 COMPUTER READABLE FORM:

```

1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Version #1.25
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/08/397,633A
7      FILING DATE:
8      CLASSIFICATION: 530
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Rowland, Bertram I
11     REGISTRATION NUMBER: 20,015
12     REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: (415) 781-1989
15     TELEFAX: (415) 398-3249
16     TELEX: 910 277299
17     INFORMATION FOR SEQ ID NO: 68:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 884 amino acids
20     TYPE: amino acid
21     STRANDEDNESS: single
22     TOPOLOGY: linear
23     MOLECULE TYPE: protein
24     US-08-397-633A-68

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Query Match	Score	DB 1	Length
	82.6%	3448	884

Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	58
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	93
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	114
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	153
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	170
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	213
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	227
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	273
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	283
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	333
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	340
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	393
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	453
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	513
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	566
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	622
QY	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	633
Db	GAAGAGAGAGGVCPTGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	693

[illegible]

RESULT 3
US-08-435-641-15
; Sequence 15, Application US/08435641

GENERAL INFORMATION:
APPLICANT: Steidronsky, Erwin R.
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
TITLE OF INVENTION: Crosslinking
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleh, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,641
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-61127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-435-641-15

Query Match	82.6%;	Score 3448;	DB 2;	Length 884;
Best Local Similarity	90.6%;	Pred. NO. 1.8e-246;		
Matches 752; Conservative	0;	Mismatches 26;	Indels 52;	Gaps 52

QY	3	GAGSAGAGSGGTVGVPGVGPBGKGV-PGVG - PGVG - PGVG - PGAGAGSAGA	58
Dd	34	GAGSGAGSGSVGVPGVGPBGVPBGKGPBGVGPBGVGPBGVGPBGAGSAGAG	93
QY	59	GSAGAGSGAGSGSSGVPGVGPBGVGPBGKGV-PGVG - PGVG - PGVG - PGAGAGS	114
Dd	94	GSGAGAGSGAGAGSGGVPGVGPBGVGPBGKGVPGVGPBGVGPBGVGPBGAGAGS	153
QY	115	GAGAGSGAGAGSGAGAGSGGVGPBGVGPBGVGPBGKVPBGV - PGVG - PGVG - PGA	170
Dd	154	GAGAGSGAGAGSGAGAGSGGVPGVGPBGVGPBGKVPBGVGPBGVGPBGVPGA	213
QY	171	GAGSGAGAGSGAGAGSAGAGSGGVPGVGPBGVGPBGKGVPGV - PGVG - PGVG - PGVG	227
Dd	214	GAGSGAGAGSGAGAGSAGAGSGGVPGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGV	273

Oy		222	-	PAGAGSGAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgvg-	-pgvg-	28.93	
Db		274	vPgAGGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgvg-		33.33		
Oy		284	pGVG-	pGAGSGAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgvg-	-pgvg- p	34.04	
Db		334	pGvgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgvg-		39.93		
Oy		341	GVC-	pGVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgvg-	PG	39.97
Db		394	GvGvpGvgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpg-		45.33		
Oy		398	VG-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgv	45.44
Db		454	vGvPgVgtvPvgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgk		51.33		
Oy		455	G-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgkcvpgk	51.10
Db		514	GvtpGvtpGvgtvPgVgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgvg		57.33		
Oy		511	vPgvg-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgvpgvg	56.66
Db		574	vPgkGvPgVgtvPgVgtvPgVgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgv		63.33		
Oy		567	pGkGvtpGvg-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgv	62.22
Db		634	pGvgtvPgkGvtpGvgtvPgVgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgv		69.33		
Oy		623	GvGvpPgkGvPgvg-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgv	67.87
Db		694	GvGvtpGvgtvPgkGvtpGvgtvPgVgtvPgAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgv		75.33		
Oy		679	vGvPgVgtvPgkGvtpGvg-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGAGSAGGvgtcvtgpcgv	73.44
Db		754	vGvPgVgtvPgVgtvPgkGvtpGvgtvPgVgtvPgAGAGSAGAGSAGAGSAGGvgtcvtgpcgv		81.33		
Oy		735	GvtpGvtpPgVgtvPgkGvtpGvg-	-pgvg-	-pgVG-	pGAGAGSAGAGSAGAGSAGGvgtcvtgpcgv	78.80
Db		814	GvtpGvtpPgVgtvPgVgtvPgkGvtpGvgtvPgVgtvPgAGAGSAGAGSAGGvgtcvtgpcgv		86.33		

RESULT 4
US-08-707-237A-96
; Sequence 96, Application US/08707237A
; Patent No. 5830713

GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Capello, Joseph
APPLICANT: Cissman, John W.
APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleh, Hobach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,237A
FILING DATE: 03-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA: 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA: 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA: 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA: 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-707-237A-96

Query Match 82.6%; Score 3448; DB 2; Length 884;
Best Local Similarity 90.6%; Pred. No. 1.8e-246;

Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGPVGVPGVPGKGVPGV-G-PGVG-PGVG-PGAGAGSAGA 58
DB 34 GAGSGAGAGSGVGPVGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGV 93
QY 59 GSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV-G-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGV 153
QY 115 GAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV-G-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVPGVPGVPGVPGV 213
QY 171 GAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV-G-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVPGVPGVPGVPGVPGV 273
QY 228 -PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV-G-PGVG-PGVG- 283
DB 274 VEGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVPGVPGVPGV 333
QY 284 PGV-G-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV-G-PGVG-P 340
DB 334 PGVGPVPGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVPGVPGV 353
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV-PG 397
DB 394 GVGPGVPGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGVPGVPGVPGVPG 453
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV 454
DB 454 VGVPGVPGVGPVPGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGVPGVPGK 513
QY 455 G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGVPGVPGK 510
DB 514 GVPVGPVPGVGPVPGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGVPGVPG 573
QY 511 VGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGVPGV 566

DB 574 VPGKGVPGVGPVGPVPGVPGAGAGSGAGAGSGAGAGSGVGPVGPVGPV 633
QY 567 PGKGVPGV-G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGPV 622
DB 634 PGVGPVPGKGVPGVGPVPGVPGAGAGSGAGAGSGAGAGSGVGPVGPV 693
QY 623 GVGPGKGVPGV-G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPV 678
DB 694 GVGPGVPGVPGKGVPGVGPVPGVPGVPGAGAGSGAGAGSGAGAGSGV 753
QY 679 VGVPGVPGKGVPGV-G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 754 VGVPGVPGVGPVPGKGVPGVGPVPGVPGVPGAGAGSGAGAGSGAGAGSGV 813
QY 735 GVPVGPVPGVGPVPGKGVPGV-G-PGVG-PGVG-PGAGAGSGAGAGS 780
DB 814 GVPVGPVPGVGPVPGKGVPGVGPVPGVPGVPGAGAGSGAGAGS 863

RESULT 5

US-08-642-246-15
Sequence 15, Application US/08642246

Patent No. 6033654
GENERAL INFORMATION:

APPLICANT: STEDRONSKY, Erwin R.

TITLE OF INVENTION: Tissue Adhesive Using Synthetic

TITLE OF INVENTION: Crosslinking

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: Four Embarcadero Center, Suite 200

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/642,246

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOWLAND, Bettam I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A61127-1/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 884 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-642-246-15

Query Match 82.6%; Score 3448; DB 3; Length 884;
Best Local Similarity 90.6%; Pred. No. 1.8e-246;

Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGPVGPVPGKGVPGV-G-PGVG-PGVG-PGAGAGSAGA 58
DB 34 GAGSGAGAGSGVGPVGPVPGVPGKGVPGVPGVPGVPGVPGVPGVPGV 93
QY 59 GSGAGAGSGAGAGSGVGPVGPVPGKGVPGV-G-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGAGSGVGPVGPVPGVPGKGVPGVPGVPGVPGVPGVPGAGS 153


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RESULT 9
US-08-477-509B-82
: Sequence 82: Application US/08477509B
: Patent No. 5770697
: GENERAL INFORMATION:
: APPLICANT: Ferrari, Franco A
: APPLICANT: Cappello, Joseph
: APPLICANT: Crisman, John W
: APPLICANT: Dorman, Mary A
: TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
: TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
: NUMBER OF SEQUENCES: 112
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,509B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/175,155
: FILING DATE: 29-DEC-1993
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/053,049
: FILING DATE: 22-APR-1993
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/114,618
: FILING DATE: 29-OCT-1987
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/927,258
: FILING DATE: 04-NOV-1986
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Treccartin, Richard F.
: REGISTRATION NUMBER: 31,801
: REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-781-1989
: TELEFAX: 415-398-3249
:
: INFORMATION FOR SEQ ID NO: 82:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2257 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide

```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-27

Query Match 78.0%; Score 3253; DB 3; Length 832;
Best Local Similarity 88.9%; Pred. No. 3.6e-232;
Matches 742; Conservative 0; Mismatches 13; Indels 80; Gaps 65;

QY 9 GAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGSGAGAG 65
DB 3 G---VGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV-GAGAGSGAGAGSGAGAG 57
QY 66 SGAGAGS--GVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGS 120
DB 58 SGAGAGSVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV-GAGAGSGAGAGS 116
QY 121 GAGAGSGAGAGS--GVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSG 175
DB 117 GAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV-GAGAGSG 175
QY 176 AGAGSGAGAGSGAGAGS--GVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGA 230
DB 176 AGAGSGAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV-GA 234
QY 231 GAGSGAGAGSGAGAGSGAGAGS--GVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PG 285
DB 235 GAGSGAGAGSGAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPG 294
QY 286 VGPAGAGSGAGAGSGAGAGSGAGAGS--GVGVPGVGVPGVGVPGKGVPGVG-PGVG-PG 341
DB 295 VG-GAGAGSGAGAGSGAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVPGVGVPG 353
QY 342 VG-PGVGPGAGAGSGAGAGSGAGAGSGAGAGS--GVGVPGVGVPGVGVPGKGVPGVG-PG 397
DB 354 VGVPGVG-GAGAGSGAGAGSGAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVPGV 412
QY 398 VG-PGVG-PGVGPGAGAGSGAGAGSGAGAGSGAGAGS--GVGVPGVGVPGVGVPGKGVPG 453
DB 413 VGVPGVGVPGVG-GAGAGSGAGAGSGAGAGSGAGAGSVPGVGVPGVGVPGVGVPGV 471
QY 454 VG-PGVG-PGVGPGAGAGSGAGAGSGAGAGSGAGAGS--GVGVPGVGVPGVGVPG 508
DB 472 VGVPGVGVPGVG-PGVG-GAGAGSGAGAGSGAGAGSGAGAGSVPGVGVPGVGVPG 530
QY 509 KGVPGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGSGAGAGS--GVGVPGVGVPG 563
DB 531 VGVPGVGVPGVGPGVGVPGVG-GAGAGSGAGAGSGAGAGSGAGAGSVPGVGVPGVPG 589
QY 564 VGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGSGAGAGS--GVGVPG 618
DB 590 VGVPGVGVPGVGPGVGVPGVGPGVG-GAGAGSGAGAGSGAGAGSGAGAGSVPGVGVPG 648

QY 619 VGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGS--G 673
DB 649 VGVPGVGVPGVGPGVGVPGVGPGVGVPGVGVPGVGVPGV-GAGAGSGAGAGSGAGAGSVPG 707
QY 674 VGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAG 730
DB 708 VGVPGVGVPGVGPGVGVPGVGPGVGVPGVGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAG 766
QY 731 GS--GVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGS 780
DB 767 GSVPGVGVPGVGVPGVGVPGVGPGVGVPGVGVPGVGVPGVGVPGVGVPGV-GAGAGSGAGAGS 820

Search completed: December 30, 2004, 12:58:12
Job time : 33 secs

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OY	121	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	180
Dd	121	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	180
OY	181	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	240
Dd	181	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	240
OY	241	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	300
Dd	241	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	300
OY	301	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	360
Dd	301	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	360
OY	361	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	420
Dd	361	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	420
OY	421	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	480
Dd	421	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	480
OY	481	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	540
Dd	481	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	540
OY	541	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	600
Dd	541	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	600
OY	601	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	660
Dd	601	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	660
OY	661	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	720
Dd	661	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	720
OY	721	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	780
Dd	721	GAGAGSSGAGAGSGVGPVGVPGVGVPGPKGVPGVGPBGKVPBGVPGVPGPVGGAGAAGSAGAAGS	780
RESULT 2			
US-10-800-179-19			
; Sequence 19, Application US/10800179			
; Publication No. US20040180027A1			
GENERAL INFORMATION:			
APPLICANT: Chevas, William A.			
APPLICANT: Kumar, Manoj			
TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care			
FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074			
CURRENT APPLICATION NUMBER: US/10/800,179			
PRIOR FILING DATE: 2004-03-12			
PRIOR APPLICATION NUMBER: 60/454,077			
PRIOR FILING DATE: 2003-03-12			
NUMBER OF SEQ ID NOS: 31			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 19			
LENGTH: 780			
TYPE: PRT			
ORGANISM: Unknown			
FEATURE:			
OTHER INFORMATION: SLP 47K			
US-10-800-179-19			

Query Match	100.0%;	Score 4173;	DB 16;	Length 780;
Best Local Similarity	100.0%;	Pred. No. 8.9e-248;		
Matches 780;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

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/ RESULT 3
/ US-10-845-775A-19
/ Sequence 19, Application US/10845775A
/ Publication No. US20040228913A1
/ GENERAL INFORMATION:
/ APPLICANT: Kumar, Manoj
/ APPLICANT: Mazeaud, Isabelle
/ APPLICANT: Christiano, Steven P.
/ TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequences
/ FILE REFERENCE: Protein Polymers
/ FILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
/ CURRENT APPLICATION NUMBER: US/10/845,775A
/ CURRENT FILING DATE: 2004-05-14
/ PRIOR APPLICATION NUMBER: US 60/470,465
/ PRIOR FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
/ LENGTH: 780
/ TYPE: PRT
/

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[illegible]

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Db      394  GVGVPGVPGAGAGSAGAGSAGAGSAGAGSGVGVPGVGVPGVGVPGV 453
Qy      398  VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGV 454
Db      454  VGVPGVGVPGVGVPGAGAGSAGAGSAGAGSGAGAGSGVGVPGVGVPGV 513
Qy      455  G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVGVPGVPGK 510
Db      514  GVPGVGVPGVGVPGVVPFGAGAGSGAGAGSGAGAGSGVGVPGVGVPGV 573
Qy      511  VPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVGVPGVPGV 566
Db      574  VPGVGVPGVGVPGVGVPGVGVPGAGAGSGAGAGSGAGAGSGVGVPGV 633
Qy      567  PGKGVPGV-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVPG 622
Db      634  PGVGVPGVGVPGVGVPGVGVPGVPGAGAGSGAGAGSGAGAGSGVGV 693
Qy      623  GVGVPKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 678
Db      694  GVGPGVGVPGVGVPGVGVPGVGVPGVGVPGAGAGSGAGAGSGAGAGSG 753
Qy      679  VGVPGVGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 744
Db      754  VGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVVPFGAGAGSGAGAGSGAGAGSGV 813
Qy      735  GVPGVGVPGVGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
Db      814  GVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVPGAGAGSGAGAGS 863

RESULT 6
; US-10-117-931-15
; Sequence 15, Application US/10117931
; Publication No. US20030104589A1
; GENERAL INFORMATION:
APPLICANT: STEBRONSKY, Et*in R.
CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRIGHTON & HERBERT
STREET: Four Embardadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/117,931
FILING DATE: 05-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/642,246
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-396-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-117-931-15

Query Match 82.6%; Score 3448; DB 14; Length 884;
Best Local Similarity 90.6%; Pred. No. 1.9e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

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QY 3 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB |||||
DB 34 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB |||||
DB 94 GSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 153
QY 115 GAGAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGA 213
QY 171 GAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 273
QY 228 -PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 283
DB 274 VPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 333
QY 284 PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-P 340
DB 334 PGVGPGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 393
QY 341 GVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PG 397
DB 394 GVGPGVGPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 453
QY 398 VG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 454
DB 454 VGVPGVGPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 513
QY 455 G-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 510
DB 514 GVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 573
QY 511 VPGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 566
DB 574 VPGKVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 633
QY 567 PGKVPVGVP-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 622
DB 634 PGVGPVGKVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 693
QY 623 GVGVPVGKVPVGVP-PGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 678
DB 694 GVGVPVGKVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 753
QY 679 VGVPGVGPVGKVPVGVP-PGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 734
DB 754 VGVPGVGPVGVPVGKVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 813
QY 735 GVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 780
DB 814 GVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 863
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RESULT 7
US-10-800-179-25
; Sequence 25, Application US/10800179
; Publication No. US20040180027A1
; GENERAL INFORMATION:
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj
; TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care

; TITLE OF INVENTION: Compositions
; FILE REFERENCE: DOC 0057 PA / GCT92-4 / DC 5074
; CURRENT APPLICATION NUMBER: US/10/800,179
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,077
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 884
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: SELL 47E-13
US-10-800-179-25

Query Match 82.6%; Score 3448; DB 16; Length 884;
Best Local Similarity 90.6%; Pred. No. 1.9e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

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QY 3 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB |||||
DB 34 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB |||||
DB 94 GSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 153
QY 115 GAGAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGA 213
QY 171 GAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 273
QY 228 -PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 283
DB 274 VPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 333
QY 284 PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-P 340
DB 334 PGVGPGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 393
QY 341 GVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PG 397
DB 394 GVGPGVGPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 453
QY 398 VG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 454
DB 454 VGVPGVGPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 513
QY 455 G-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 510
DB 514 GVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 573
QY 511 VPGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 566
DB 574 VPGKVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 633
QY 567 PGKVPVGVP-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 622
DB 634 PGVGPVGKVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 693
QY 623 GVGVPVGKVPVGVP-PGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 678
DB 694 GVGVPVGKVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 753
QY 679 VGVPGVGPVGKVPVGVP-PGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 734
DB 754 VGVPGVGPVGVPVGKVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 813
QY 735 GVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGVG 780
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QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVPGKGVPGV 454
DB 454 VGVPGVGBGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGVPGV 513
QY 455 G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGK 510
DB 514 GVPGVPGVGBGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGV 573
QY 511 VGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVPGV 566
DB 574 VGBGVPGVGBGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGV 633
QY 567 PGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGV 622
DB 634 PGVPGVGBGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGVGVPGV 693
QY 623 GVGPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVPG 678
DB 694 GVGPGVPGVGBGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGVPG 753
QY 679 VGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 754 VGVPGVPGVGBGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGV 813
QY 735 GVPGVPGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
DB 814 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGAGAGSGAGAGS 863

RESULT 10

US-10-845-936A-37
Sequence 37, Application US/10845936A
Publication No. US20040234609A1
GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
TITLE OF INVENTION: and Uses
FILE REFERENCE: DOC0068PA/DC5058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37
LENGTH: 983
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: CBPexamer-SELP47K: silk, elastin and cellulose binding peptide
US-10-845-936A-37

Query Match 82.6%; Score 3448; DB 17; Length 983;
Best Local Similarity 90.6%; Pred. No. 2e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
QY 3 GAGSGAGAGSGVPGVPGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 133 GAGSGAGAGSGVPGVPGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGAGAGSGAGA 192
QY 59 GSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGS 114
DB 199 GSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGAGAGS 252
QY 115 GAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGA 170
DB 253 GAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGA 312
QY 171 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV-PGVG-PGVG-PGVG 227

DB 313 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGVPGVPGV 372
QY 228 -PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV-PGVG-PGVG- 283
DB 373 VPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 432
QY 284 PGVPG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV-PGVG-P 340
DB 433 PGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGV 492
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGV-PG 397
DB 493 GVGPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPG 552
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGKGVPGV 454
DB 553 VGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGK 612
QY 455 G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGV 672
DB 613 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 672
QY 511 VPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGV 566
DB 673 VPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 732
DB 733 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 792
QY 623 GVGPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGV 678
DB 793 GVGPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 852
QY 679 VGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGV 734
DB 853 VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 912
QY 735 GVPGVPGVPGVPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
DB 913 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 962

RESULT 11

US-10-845-936A-32
Sequence 32, Application US/10845936A
Publication No. US20040234609A1
GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
TITLE OF INVENTION: and Uses
FILE REFERENCE: DOC0068PA/DC5058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 1027
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: silk and elastin and cecropin A melittin peptide repeat sequence:
US-10-845-936A-32

Query Match 82.6%; Score 3448; DB 17; Length 1027;
Best Local Similarity 90.6%; Pred. No. 2.1e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;


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Publication No. US20040234609A1
GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
FILE REFERENCE: DOC00689A/DC5058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 1125
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: GFP-SELP47K: blk, elastin and green fluorescent protein peptides
US-10-845-936A-34

Query Match      82.6%; Score 3448; DB 17; Length 1125;
Best Local Similarity 90.6%; Pred. No. 2.3e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGAGAGSGAGA 58
DB 275 GAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGAGAGSGAGA 334
QY 59 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGAGAGS 114
DB 335 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGAGAGS 394
QY 115 GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGA 170
DB 395 GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGA 454
QY 171 GAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGVG 227
DB 455 GAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGVG 514
QY 228 -PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG-- 283
DB 515 VPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG-- 574
QY 284 PGVG--PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--P 340
DB 575 PGVGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--P 634
QY 341 GVG--PGVG--PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PG 397
DB 635 GVGVPGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG 694
QY 398 VG--PGVG--PGVG--PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGV 454
DB 655 VGVPGVGVPGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGV 754
QY 455 G--PGVG--PGVG--PGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGK 510
DB 755 GVPGVGVPGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG 814
QY 511 VPGVG--PGVG--PGVG--PGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGV 566
DB 815 VPGKGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGV 874
QY 567 PGKGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGV 622
DB 875 PGKGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGV 934
QY 623 GVGVPKGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGV 678
DB 935 GVGVPKGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGV 994
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QY 679 VGVPGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGV 734
DB 995 VGVPGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGV 1054
QY 735 GVGVPVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGV 780
DB 1055 GVGVPVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGV 1104

RESULT 14
US-10-800-179-31
Sequence 31, Application US/10800179
Publication No. US20040180027A1
GENERAL INFORMATION:
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj
TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care
FILE REFERENCE: DOC 0057PA / GC792-4 / DC 5074
CURRENT APPLICATION NUMBER: US/10/800,179
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/454,077
PRIOR FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 965
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: SELP 58
US-10-800-179-31

Query Match      80.2%; Score 3346; DB 16; Length 965;
Best Local Similarity 82.9%; Pred. No. 3.4e-197;
Matches 744; Conservative 0; Mismatches 33; Indels 120; Gaps 52;

QY 4 AGSGAGAG--SGVGVPGVGVPGVGVPGKGVPGVG--PGVG--PGV---GPGVPGAAGAGSGAG 57
DB 29 ASDPMGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVPGAAGAGSGAGSGAG 88
QY 58 AGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG--PGVG--PGVG--PGV-----G 107
DB 89 AGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVPGAAGAG 148
QY 108 PGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVPGAAGAGSGAG--PGVG--PGVG--P 164
DB 149 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVPGAAGAGSGAG--PGVG--PGVG--P 208
QY 165 GV-----GPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVPGAAGAGSGAG--PGVG--PGVG--P 216
DB 209 GVGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 268
QY 217 GVG--PGVG--PGV-----GPGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 267
DB 269 GVGVPVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 328
QY 268 GKGVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 317
DB 329 GVGVPVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 388
QY 318 GVGVPVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 367
DB 389 GVGVPVPGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 448
QY 368 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 417
DB 449 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 508
QY 418 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 467
DB 509 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAG--PGVG--PGVG--P 568
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Qy	468	PGAGSGAGAGAGSGAAGAGSGAGAGSGGTVGVPGVGVPKGKVPVG--PGVG--PGVG--P	52.4
Db	569	SGAGAGSGAGAGSGAGAGSGAGAGSGGTVGVPGVGVPGVGVPGVGVPGVGVP	62.88
Qy	525	GV-----GPGAGAGSGAGAGSGAGAGSGAGAGSGGTVGVPGVGVPKGKVPVG--P	57.66
Db	629	GTVGVPAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGGTVGVPGVGVPGVGVP	66.88
Qy	577	GVG--PGVG--PGV-----GPGAAGAGSGAGAGSGAGAGSGAGAGSGGTVGVPGVGVP	62.77
Db	689	GTVGVPGVGVPGVGVPAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGGTVGVPGVGVP	74.8
Qy	628	GKGVPGVG--PGVG--PGVG--PGV-----GPGAAGAGSGAGAGSGAGAGSGGTVGVP	67.77
Db	749	GTVGVPGVGVPGVGVPGVGVPAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGGTVGVP	80.8
Qy	678	GTVGVPGVGVPKGKVPVG--PGVG--PGVG--PGV-----GPGAAGAGSGAGAGSG	72.77
Db	809	GTVGVPGVGVPGVGVPGVGVPGVGVPGVGVPAGAGSGAGAGSGAGAGSG	86.88
Qy	728	AGAGSGVPGVPGVPGVPGVPGKVPVG--PGVG--PGVG--PGVG--PGAAGAGAGAGS	78.0
Db	869	AGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGAGAGSGAGAGS	92.5

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RESULT 15
US-10-845-775A-31
; Sequence 31, Application US/10845775A
; Publication No. US20040228913A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Manoj
; APPLICANT: Mazaed, Isabelle
; APPLICANT: Christiano, Steven P.
; TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequence
; TITLE OF INVENTION: Protein Polymers
; FILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
; CURRENT APPLICATION NUMBER: US/10/845,775A
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/470,465
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 965
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: silk and elastin peptides
US-10-845-775A-31

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Query Match	80.2%;	Score 3346;	DB 17;	Length 965;
Best Local Similarity	82.9%;	Pred. No. 3,4e-197;		
Matches 744;	Conservative	0;	Mismatches 33;	Indels 120; Gaps 52;

QY	4	AASGAGAG--SGVGPVGVPVGPVPGKGVPGV--PGVG--PGV---GPGVPPGAGAGSGAG	57
Db	29	AADPMGVGVPGVGPVPGVGPVPGVGPVPGVGPVPGVGPVPGVGPVPGAGAGSGAGAGSGAG	88
QY	58	AGSGAGAGSGAGAGSGVGVPGVGPVGVPGVPGKGVPGVG--PGVG--PGV-----G	107
Db	89	AASGAGAGSGAGAGSGVGPVGPVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVPGAGAG	148
QY	108	PGAGAGSGAGAGSGAGAGSGAGSGVGPVGPVGPVGPVPGKGVPGVG--PGVG--PGVG--P	164
Db	149	SGAGAGSGAGAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV	208
QY	165	GV-----GPAGAGSGAGAGSGAGAGSGAGSGVGPVGPVGPVGPVPGKGVPGVG--P	216
Db	209	GVGPVPGAGAGSGAGAGSGAGAGSGAGAGSGAGSGVGPVGPVGPVGPVGPVGPVGPVGPV	268
QY	217	GVG--PGVG--PGV-----GPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGPVGPVGPV	267

[illegible]

Search completed: December 30, 2004, 13:01:33
Job time : 154 secs